Product and Method

The present invention relates to oligonucleotide probes, for use in assessing gene transcript levels in a cell, which may be used in analytical techniques, particularly diagnostic techniques. Conveniently the probes are provided in kit form. Different sets of probes may be used in techniques to prepare gene expression patterns and identify, diagnose or monitor different states, such as diseases, conditions or stages thereof. Also provided are methods of identifying suitable probes and their use in methods of the invention.

The identification of quick and easy methods of sample analysis for, for example, diagnostic applications, remains the goal of many researchers. End users seek methods which are cost effective, produce statistically significant results and which may be implemented routinely without the need for highly skilled individuals.

The analysis of gene expression within cells has been used to provide information on the state of those cells and importantly the state of the individual from which the cells are derived. The relative expression of various genes in a cell has been identified as reflecting a particular state within a body. For example, cancer cells are known to exhibit altered expression of various proteins and the transcripts or the expressed proteins may therefore be used as markers of that disease state.

Thus biopsy tissue may be analysed for the presence of these markers and cells originating from the site of the disease may be identified in other tissues or fluids of the body by the presence of the markers. Furthermore, products of the altered expression may be

released into the blood stream and these products may be analysed. In addition cells which have contacted disease cells may be affected by their direct contact with those cells resulting in altered gene expression and their expression or products of expression may be similarly analysed.

However, there are some limitations with these methods. For example, the use of specific tumour markers for identifying cancer suffers from a variety of defects, such as lack of specificity or sensitivity, association of the marker with disease states besides the specific type of cancer, and difficulty of detection in asymptomatic individuals.

In addition to the analysis of one or two marker transcripts or proteins, more recently, gene expression patterns have been analysed. Most of the work involving large-scale gene expression analysis with implications in disease diagnosis has involved clinical samples originating from diseased tissues or cells. For example, several recent publications, which demonstrate that gene expression data can be used to distinguish between similar cancer types, have used clinical samples from diseased tissues or cells (Alon et al. 1999, PNAS, 96, p6745-6750; Golub et al. 1999, Science, 286, p531-537; Alizadeh et al, 2000, Nature, 403, p503-511; Bittner et al., 2000, Nature, 406, p536-540).

However, these methods have relied on analysis of a sample containing diseased cells or products of those cells or cells which have been contacted by disease cells. Analysis of such samples relies on knowledge of the presence of a disease and its location, which may be difficult in asymptomatic patients. Furthermore, samples can not always be taken from the disease site, e.g. in diseases of the brain.

In a finding of great significance, the present inventors identified the previously untapped potential of all cells within a body to provide information

relating to the state of the organism from which the cells were derived. WO98/49342 describes the analysis of the gene expression of cells distant from the site of disease, e.g. peripheral blood collected distant from a cancer site.

This finding is based on the premise that the different parts of an organism's body exist in dynamic interaction with each other. When a disease affects one part of the body, other parts of the body are also affected. The interaction results from a wide spectrum of biochemical signals that are released from the diseased area, affecting other areas in the body. Although, the nature of the biochemical and physiological changes induced by the released signals can vary in the different body parts, the changes can be measured at the level of gene expression and used for diagnostic purposes.

The physiological state of a cell in an organism is determined by the pattern with which genes are expressed in it. The pattern depends upon the internal and external biological stimuli to which said cell is exposed, and any change either in the extent or in the nature of these stimuli can lead to a change in the pattern with which the different genes are expressed in the cell. There is a growing understanding that by analysing the systemic changes in gene expression patterns in cells in biological samples, it is possible to provide information on the type and nature of the biological stimuli that are acting on them. Thus, for example, by monitoring the expression of a large number of genes in cells in a test sample, it is possible to determine whether their genes are expressed with a pattern characteristic for a particular disease, condition or stage thereof. Measuring changes in gene activities in cells, e.g. from tissue or body fluids is therefore emerging as a powerful tool for disease diagnosis.

- 4 -

Such methods have various advantages. Often, obtaining clinical samples from certain areas in the body that is diseased can be difficult and may involve undesirable invasions in the body, for example biopsy is
5   often used to obtain samples for cancer. In some cases, such as in Alzheimer's disease the diseased brain specimen can only be obtained post-mortem. Furthermore, the tissue specimens which are obtained are often heterogeneous and may contain a mixture of both diseased
10   and non-diseased cells, making the analysis of generated gene expression data both complex and difficult.

It has been suggested that a pool of tumour tissues that appear to be pathogenetically homogeneous with respect to morphological appearances of the tumour may
15   well be highly heterogeneous at the molecular level (Alizadeh, 2000, supra), and in fact might contain tumours representing essentially different diseases (Alizadeh, 2000, supra; Golub, 1999, supra). For the purpose of identifying a disease, condition, or a stage
20   thereof, any method that does not require clinical samples to originate directly from diseased tissues or cells is highly desirable since clinical samples representing a homogeneous mixture of cell types can be obtained from an easily accessible region in the body.

25   We have now identified a set of probes of surprising utility for identifying one or more diseases. Thus, we now describe probes and sets of probes derived from cells which are not disease cells and which have not contacted disease cells, which correspond to genes
30   which exhibit altered expression in normal versus disease individuals, for use in methods of identifying, diagnosing or monitoring certain conditions, particularly diseases or stages thereof.

Thus the invention provides a set of
35   oligonucleotide probes which correspond to genes in a cell whose expression is affected in a pattern characteristic of a particular disease, condition or

stage thereof, wherein said genes are systemically affected by said disease, condition or stage thereof. Preferably said genes are metabolic or house-keeping genes and preferably are constitutively moderately or highly expressed. Preferably the genes are moderately or highly expressed in the cells of the sample but not in cells from disease cells or in cells having contacted such disease cells.

Such probes, particularly when isolated from cells distant to the site of disease, do not rely on the development of disease to clinically recognizable levels and allow detection of a disease or condition or stage thereof very early after the onset of said disease or condition, even years before other subjective or objective symptoms appear.

As used herein "systemically" affected genes refers to genes whose expression is affected in the body without direct contact with a disease cell or disease site and the cells under investigation are not disease cells.

"Contact" as referred to herein refers to cells coming into close proximity with one another such that the direct effect of one cell on the other may be observed, e.g. an immune response, wherein these responses are not mediated by secondary molecules released from the first cell over a large distance to affect the second cell. Preferably contact refers to physical contact, or contact that is as close as is sterically possible, conveniently, cells which contact one another are found in the same unit volume, for example within 1cm^3.

A "disease cell" is a cell manifesting phenotypic changes and is present at the disease site at some time during its life-span, e.g. a tumour cell at the tumour site or which has disseminated from the tumour, or a brain cell in the case of brain disorders such as Alzheimer's disease.

- 6 -

"Metabolic" or "house-keeping" genes refer to those genes responsible for expressing products involved in cell division and maintenance, e.g. non-immune function related genes.

5   "Moderately or highly" expressed genes refers to those present in resting cells in a copy number of more than 30-100 copies/cell (assuming an average $3x10^5$ mRNA molecules in a cell).

Specific probes having the above described
10   properties are provided herein.

Thus in one aspect, the present invention provides a set of oligonucleotide probes, wherein said set comprises at least 10 oligonucleotides selected from:

an oligonucleotide as described in Table 1 or
15   derived from a sequence described in Table 1, or an oligonucleotide with a complementary sequence, or a functionally equivalent oligonucleotide.

"Table 1" as referred to herein refers to Table 1a and/or Table 1b. Table 1b contains reference to
20   additional clones and sequences as disclosed herein. Similarly Tables 2 and 4 comprise 2 parts, a and b.

The invention also provides one or more oligonucleotide probes, wherein each oligonucleotide probe is selected from the oligonucleotides listed in
25   Table 1, or derived from a sequence described in Table 1, or a complementary sequence thereof. The use of such probes in products and methods of the invention, form further aspects of the invention.

As referred to herein an "oligonucleotide" is a
30   nucleic acid molecule having at least 6 monomers in the polymeric structure, ie. nucleotides or modified forms thereof. The nucleic acid molecule may be DNA, RNA or PNA (peptide nucleic acid) or hybrids thereof or modified versions thereof, e.g. chemically modified
35   forms, e.g. LNA (Locked Nucleic acid), by methylation or made up of modified or non-natural bases during synthesis, providing they retain their ability to bind

to complementary sequences. Such oligonucleotides are used in accordance with the invention to probe target sequences and are thus referred to herein also as oligonucleotide probes or simply as probes.

An "oligonucleotide derived from a sequence described in Table 1" (or any other table) refers to a part of a sequence disclosed in that Table (e.g. Table 1-4), which satisfies the requirements of the oligonucleotide probes as described herein, e.g. in length and function. Preferably said parts have the size described hereinafter.

Preferably the oligonucleotide probes forming said set are at least 15 bases in length to allow binding of target molecules. Especially preferably said oligonucleotide probes are from 20 to 200 bases in length, e.g. from 30 to 150 bases, preferably 50-100 bases in length.

As referred to herein the term "complementary sequences" refers to sequences with consecutive complementary bases (ie. T:A, G:C) and which complementary sequences are therefore able to bind to one another through their complementarity.

Reference to "10 oligonucleotides" refers to 10 different oligonucleotides. Whilst a Table 1 oligonucleotide, a Table 1 derived oligonucleotide and their functional equivalent are considered different oligonucleotides, complementary oligonucleotides are not considered different. Preferably however, the at least 10 oligonucleotides are 10 different Table 1 oligonucleotides (or Table 1 derived oligonucleotides or their functional equivalents). Thus said 10 different oligonucleotides are preferably able to bind to 10 different transcripts.

Preferably said oligonucleotides are as described in Table 1 or are derived from a sequence described in Table 1. Especially preferably said oligonucleotides are as described in Table 2 or Table 4 or are derived

- 8 -

from a sequence described in either of those tables.
Especially preferably the oligonucleotide (or the
oligonucleotide derived therefrom) has a high occurrence
as defined in Table 3, especially preferably >40%, e.g.
>80 or >90, e.g. 100%.

A "set" as described refers to a collection of
unique oligonucleotide probes (ie. having a distinct
sequence) and preferably consists of less than 1000
oligonucleotide probes, especially less than 500 probes,
e.g. preferably from 10 to 500, e.g. 10 to 100, 200 or
300, especially preferably 20 to 100, e.g. 30 to 100
probes. In some cases less than 10 probes may be used,
e.g. from 2 to 9 probes, e.g. 5 to 9 probes.

It will be appreciated that increasing the number
of probes will prevent the possibility of poor analysis,
e.g. misdiagnosis by comparison to other diseases which
could similarly alter the expression of the particular
genes in question. Other oligonucleotide probes not
described herein may also be present, particularly if
they aid the ultimate use of the set of oligonucleotide
probes. However, preferably said set consists only of
said Table 1 oligonucleotides, Table 1 derived
oligonucleotides, complementary sequences or
functionally equivalent oligonucleotides, or a sub-set
thereof (e.g. of the size as described above),
preferably a sub-set for which sequences are provided
herein (see Table 1 and its footnote). Especially
preferably said set consists only of said Table 1
oligonucleotides, Table 1 derived oligonucleotides, or
complementary sequences thereof, or a sub-set thereof.

Multiple copies of each unique oligonucleotide
probe, e.g. 10 or more copies, may be present in each
set, but constitute only a single probe.

A set of oligonucleotide probes, which may
preferably be immobilized on a solid support or have
means for such immobilization, comprises the at least 10
oligonucleotide probes selected from those described

hereinbefore.   Especially preferably said probes are
selected from those having high occurrence as described
in Table 3 and as mentioned above.   As mentioned above,
these 10 probes must be unique and have different
sequences.   Having said this however, two separate
probes may be used which recognize the same gene but
reflect different splicing events.   However
oligonucleotide probes which are complementary to, and
bind to distinct genes are preferred.

As described herein a "functionally equivalent"
oligonucleotide to those described in Table 1 or derived
therefrom refers to an oligonucleotide which is capable
of identifying the same gene as an oligonucleotide of
Table 1 or derived therefrom, ie. it can bind to the
same mRNA molecule (or DNA) transcribed from a gene
(target nucleic acid molecule) as the Table 1
oligonucleotide or the Table 1 derived oligonucleotide
(or its complementary sequence).   Preferably said
functionally equivalent oligonucleotide is capable of
recognizing, ie. binding to the same splicing product as
a Table 1 oligonucleotide or a Table 1 derived
oligonucleotide.   Preferably said mRNA molecule is the
full length mRNA molecule which corresponds to the Table
1 oligonucleotide or the Table 1 derived
oligonucleotide.

As referred to herein "capable of binding" or
"binding" refers to the ability to hybridize under
conditions described hereinafter.

Alternatively expressed, functionally equivalent
oligonucleotides (or complementary sequences) have
sequence identity or will hybridize, as described
hereinafter, to a region of the target molecule to which
molecule a Table 1 oligonucleotide or a Table 1 derived
oligonucleotide or a complementary oligonucleotide
binds.   Preferably, functionally equivalent
oligonucleotides (or their complementary sequences)
hybridize to one of the mRNA sequences which corresponds

to a Table 1 oligonucleotide or a Table 1 derived
oligonucleotide under the conditions described
hereinafter or has sequence identity to a part of one of
the mRNA sequences which corresponds to a Table 1
5   oligonucleotide or a Table 1 derived oligonucleotide. A
"part" in this context refers to a stretch of at least
5, e.g. at least 10 or 20 bases, such as from 5 to 100,
e.g. 10 to 50 or 15 to 30 bases.

In a particularly preferred aspect, the
10 functionally equivalent oligonucleotide binds to all or
a part of the region of a target nucleic acid molecule
(mRNA or cDNA) to which the Table 1 oligonucleotide or
Table 1 derived oligonucleotide binds. A "target"
nucleic acid molecule is the gene transcript or related
15 product e.g. mRNA, or cDNA, or amplified product
thereof. Said "region" of said target molecule to which
said Table 1 oligonucleotide or Table 1 derived
oligonucleotide binds is the stretch over which
complementarity exists. At its largest this region is
20 the whole length of the Table 1 oligonucleotide or Table
1 derived oligonucleotide, but may be shorter if the
entire Table 1 sequence or Table 1 derived
oligonucleotide is not complementary to a region of the
target sequence.

25   Preferably said part of said region of said target
molecule is a stretch of at least 5, e.g. at least 10 or
20 bases, such as from 5 to 100, e.g. 10 to 50 or 15 to
30 bases. This may for example be achieved by said
functionally equivalent oligonucleotide having several
30 identical bases to the bases of the Table 1
oligonucleotide or the Table 1 derived oligonucleotide.
These bases may be identical over consecutive stretches,
e.g. in a part of the functionally equivalent
oligonucleotide, or may be present non-consecutively,
35 but provide sufficient complementarity to allow binding
to the target sequence.

Thus in a preferred feature, said functionally

- 11 -

equivalent oligonucleotide hybridizes under conditions
of high stringency to a Table 1 oligonucleotide or a
Table 1 derived oligonucleotide or the complementary
sequence thereof. Alternatively expressed, said
functionally equivalent oligonucleotide exhibits high
sequence identity to all or part of a Table 1
oligonucleotide. Preferably said functionally
equivalent oligonucleotide has at least 70% sequence
identity, preferably at least 80%, e.g. at least 90, 95,
98 or 99%, to all of a Table 1 oligonucleotide or a part
thereof. As used in this context, a "part" refers to a
stretch of at least 5, e.g. at least 10 or 20 bases,
such as from 5 to 100, e.g. 10 to 50 or 15 to 30 bases,
in said Table 1 oligonucleotide. Especially preferably
when sequence identity to only a part of said Table 1
oligonucleotide is present, the sequence identity is
high, e.g. at least 80% as described above.

Functionally equivalent oligonucleotides which
satisfy the above stated functional requirements include
those which are derived from the Table 1
oligonucleotides and also those which have been modified
by single or multiple nucleotide base (or equivalent)
substitution, addition and/or deletion, but which
nonetheless retain functional activity, e.g. bind to the
same target molecule as the Table 1 oligonucleotide or
the Table 1 derived oligonucleotide from which they are
further derived or modified. Preferably said
modification is of from 1 to 50, e.g. from 10 to 30,
preferably from 1 to 5 bases. Especially preferably
only minor modifications are present, e.g. variations in
less than 10 bases, e.g. less than 5 base changes.

Within the meaning of "addition" equivalents are
included oligonucleotides containing additional
sequences which are complementary to the consecutive
stretch of bases on the target molecule to which the
Table 1 oligonucleotide or the Table 1 derived
oligonucleotide binds. Alternatively the addition may

- 12 -

comprise a different, unrelated sequence, which may for example confer a further property, e.g. to provide a means for immobilization such as a linker to bind the oligonucleotide probe to a solid support.

Particularly preferred are naturally occurring equivalents such as biological variants, e.g. allelic, geographical or allotypic variants, e.g. oligonucleotides which correspond to a genetic variant, for example as present in a different species.

Functional equivalents include oligonucleotides with modified bases, e.g. using non-naturally occurring bases.   Such derivatives may be prepared during synthesis or by post production modification.

"Hybridizing" sequences which bind under conditions of low stringency are those which bind under non-stringent conditions (for example, 6x SSC/50% formamide at room temperature) and remain bound when washed under conditions of low stringency (2 X SSC, room temperature, more preferably 2 X SSC, 42°C).   Hybridizing under high stringency refers to the above conditions in which washing is performed at 2 X SSC, 65°C (where SSC = 0.15M NaCl, 0.015M sodium citrate, pH 7.2).

"Sequence identity" as referred to herein refers to the value obtained when assessed using ClustalW (Thompson et al., 1994, Nucl. Acids Res., 22, p4673-4680) with the following parameters:
Pairwise alignment parameters - Method: accurate, Matrix: IUB, Gap open penalty: 15.00, Gap extension penalty: 6.66;
Multiple alignment parameters - Matrix: IUB, Gap open penalty: 15.00, % identity for delay: 30, Negative matrix: no, Gap extension penalty: 6.66, DNA transitions weighting: 0.5.

Sequence identity at a particular base is intended to include identical bases which have simply been derivatized.

The invention also extends to polypeptides encoded

by the mRNA sequence to which a Table 1 oligonucleotide or a Table 1 derived oligonucleotide binds. The invention further extends to antibodies which bind to any of said polypeptides.

As described above, conveniently said set of oligonucleotide probes may be immobilized on one or more solid supports. Single or preferably multiple copies of each unique probe are attached to said solid supports, e.g. 10 or more, e.g. at least 100 copies of each unique probe are present.

One or more unique oligonucleotide probes may be associated with separate solid supports which together form a set of probes immobilized on multiple solid support, e.g. one or more unique probes may be immobilized on multiple beads, membranes, filters, biochips etc. which together form a set of probes, which together form modules of the kit described hereinafter. The solid support of the different modules are conveniently physically associated although the signals associated with each probe (generated as described hereinafter) must be separately determinable.

Alternatively, the probes may be immobilized on discrete portions of the same solid support, e.g. each unique oligonucleotide probe, e.g. in multiple copies, may be immobilized to a distinct and discrete portion or region of a single filter or membrane, e.g. to generate an array.

A combination of such techniques may also be used, e.g. several solid supports may be used which each immobilize several unique probes.

The expression "solid support" shall mean any solid material able to bind oligonucleotides by hydrophobic, ionic or covalent bridges.

"Immobilization" as used herein refers to reversible or irreversible association of the probes to said solid support by virtue of such binding. If reversible, the probes remain associated with the solid

- 14 -

support for a time sufficient for methods of the invention to be carried out.

Numerous solid supports suitable as immobilizing moieties according to the invention, are well known in the art and widely described in the literature and generally speaking, the solid support may be any of the well-known supports or matrices which are currently widely used or proposed for immobilization, separation etc. in chemical or biochemical procedures. Such materials include, but are not limited to, any synthetic organic polymer such as polystyrene, polyvinylchloride, polyethylene; or nitrocellulose and cellulose acetate; or tosyl activated surfaces; or glass or nylon or any surface carrying a group suited for covalent coupling of nucleic acids. The immobilizing moieties may take the form of particles, sheets, gels, filters, membranes, microfibre strips, tubes or plates, fibres or capillaries, made for example of a polymeric material e.g. agarose, cellulose, alginate, teflon, latex or polystyrene or magnetic beads. Solid supports allowing the presentation of an array, preferably in a single dimension are preferred, e.g. sheets, filters, membranes, plates or biochips.

Attachment of the nucleic acid molecules to the solid support may be performed directly or indirectly. For example if a filter is used, attachment may be performed by UV-induced crosslinking. Alternatively, attachment may be performed indirectly by the use of an attachment moiety carried on the oligonucleotide probes and/or solid support. Thus for example, a pair of affinity binding partners may be used, such as avidin, streptavidin or biotin, DNA or DNA binding protein (e.g. either the lac I repressor protein or the lac operator sequence to which it binds), antibodies (which may be mono- or polyclonal), antibody fragments or the epitopes or haptens of antibodies. In these cases, one partner of the binding pair is attached to (or is inherently

part of) the solid support and the other partner is attached to (or is inherently part of) the nucleic acid molecules.

As used herein an "affinity binding pair" refers to two components which recognize and bind to one another specifically (ie. in preference to binding to other molecules). Such binding pairs when bound together form a complex.

Attachment of appropriate functional groups to the solid support may be performed by methods well known in the art, which include for example, attachment through hydroxyl, carboxyl, aldehyde or amino groups which may be provided by treating the solid support to provide suitable surface coatings. Solid supports presenting appropriate moieties for attachment of the binding partner may be produced by routine methods known in the art.

Attachment of appropriate functional groups to the oligonucleotide probes of the invention may be performed by ligation or introduced during synthesis or amplification, for example using primers carrying an appropriate moiety, such as biotin or a particular sequence for capture.

Conveniently, the set of probes described hereinbefore is provided in kit form.

Thus viewed from a further aspect the present invention provides a kit comprising a set of oligonucleotide probes as described hereinbefore immobilized on one or more solid supports.

Preferably, said probes are immobilized on a single solid support and each unique probe is attached to a different region of said solid support. However, when attached to multiple solid supports, said multiple solid supports form the modules which make up the kit. Especially preferably said solid support is a sheet, filter, membrane, plate or biochip.

Optionally the kit may also contain information

- 16 -

relating to the signals generated by normal or diseased samples (as discussed in more detail hereinafter in relation to the use of the kits), standardizing materials, e.g. mRNA or cDNA from normal and/or diseased

5   samples for comparative purposes, labels for incorporation into cDNA, adapters for introducing nucleic acid sequences for amplification purposes, primers for amplification and/or appropriate enzymes, buffers and solutions. Optionally said kit may also

10   contain a package insert describing how the method of the invention should be performed, optionally providing standard graphs, data or software for interpretation of results obtained when performing the invention.

The use of such kits to prepare a standard

15   diagnostic gene transcript pattern as described hereinafter forms a further aspect of the invention.

The set of probes as described herein have various uses. Principally however they are used to assess the gene expression state of a test cell to provide

20   information relating to the organism from which said cell is derived. Thus the probes are useful in diagnosing, identifying or monitoring a disease or condition or stage thereof in an organism.

Thus in a further aspect the invention provides the

25   use of a set of oligonucleotide probes or a kit as described hereinbefore to determine the gene expression pattern of a cell which pattern reflects the level of gene expression of genes to which said oligonucleotide probes bind, comprising at least the steps of:

30   a) isolating mRNA from said cell, which may optionally be reverse transcribed to cDNA;

b) hybridizing the mRNA or cDNA of step (a) to a set of oligonucleotide probes or a kit as defined herein; and

35   c) assessing the amount of mRNA or cDNA hybridizing to each of said probes to produce said pattern.

The mRNA and cDNA as referred to in this method,

and the methods hereinafter, encompass derivatives or copies of said molecules, e.g. copies of such molecules such as those produced by amplification or the preparation of complementary strands, but which retain the identity of the mRNA sequence, ie. would hybridize to the direct transcript (or its complementary sequence) by virtue of precise complementarity, or sequence identity, over at least a region of said molecule. It will be appreciated that complementarity will not exist over the entire region where techniques have been used which may truncate the transcript or introduce new sequences, e.g. by primer amplification. For convenience, said mRNA or cDNA is preferably amplified prior to step b). As with the oligonucleotides described herein said molecules may be modified, e.g. by using non-natural bases during synthesis providing complementarity remains. Such molecules may also carry additional moieties such as signalling or immobilizing means.

The various steps involved in the method of preparing such a pattern are described in more detail hereinafter.

As used herein "gene expression" refers to transcription of a particular gene to produce a specific mRNA product (ie. a particular splicing product). The level of gene expression may be determined by assessing the level of transcribed mRNA molecules or cDNA molecules reverse transcribed from the mRNA molecules or products derived from those molecules, e.g. by amplification.

The "pattern" created by this technique refers to information which, for example, may be represented in tabular or graphical form and conveys information about the signal associated with two or more oligonucleotides. Preferably said pattern is expressed as an array of numbers relating to the expression level associated with each probe.

- 18 -

Preferably, said pattern is established using the following linear model:

$$y = \mathbf{X}b + f \qquad \text{Equation 1}$$

wherein, $\mathbf{X}$ is the matrix of gene expression data and y is the response variable, b is the regression coefficient vector and f the estimated residual vector. Although many different methods can be used to establish the relationship provided in equation 1, especially preferably the partial Least Squares Regression (PLSR) method is used for establishing the relationship in equation 1.

The probes are thus used to generate a pattern which reflects the gene expression of a cell at the time of its isolation. The pattern of expression is characteristic of the circumstances under which that cells finds itself and depends on the influences to which the cell has been exposed. Thus, a characteristic gene transcript pattern standard or fingerprint (standard probe pattern) for cells from an individual with a particular disease or condition may be prepared and used for comparison to transcript patterns of test cells. This has clear applications in diagnosing, monitoring or identifying whether an organism is suffering from a particular disease, condition or stage thereof.

The standard pattern is prepared by determining the extent of binding of total mRNA (or cDNA or related product), from cells from a sample of one or more organisms with the disease or condition or stage thereof, to the probes. This reflects the level of transcripts which are present which correspond to each unique probe. The amount of nucleic acid material which binds to the different probes is assessed and this information together forms the gene transcript pattern standard of that disease or condition or stage thereof. Each such standard pattern is characteristic of the disease, condition or stage thereof.

- 19 -

In a further aspect therefore, the present
invention provides a method of preparing a standard gene
transcript pattern characteristic of a disease or
condition or stage thereof in an organism comprising at
5   least the steps of:

a) isolating mRNA from the cells of a sample of one
or more organisms having the disease or condition or
stage thereof, which may optionally be reverse
transcribed to cDNA;

10   b) hybridizing the mRNA or cDNA of step (a) to a
set of oligonucleotides or a kit as described
hereinbefore specific for said disease or condition or
stage thereof in an organism and sample thereof
corresponding to the organism and sample thereof under
15   investigation; and

c) assessing the amount of mRNA or cDNA hybridizing
to each of said probes to produce a characteristic
pattern reflecting the level of gene expression of genes
to which said oligonucleotides bind, in the sample with
20   the disease, condition or stage thereof.

For convenience, said oligonucleotides are
preferably immobilized on one or more solid supports.

The standard pattern for a great number of diseases
or conditions and different stages thereof using
25   particular probes may be accumulated in databases and be
made available to laboratories on request.

"Disease" samples and organisms as referred to
herein refer to organisms (or samples from the same)
with an underlying pathological disturbance relative to
30   a normal organism (or sample), in a symptomatic or
asymptomatic organism, which may result, for example,
from infection or an acquired or congenital genetic
imperfection. Such organisms are known to have, or
which exhibit, the disease or condition or stage thereof
35   under study.

A "condition" refers to a state of the mind or body
of an organism which has not occurred through disease,

- 20 -

e.g. the presence of an agent in the body such as a toxin, drug or pollutant, or pregnancy.

"Stages" thereof refer to different stages of the disease or condition which may or may not exhibit particular physiological or metabolic changes, but do exhibit changes at the genetic level which may be detected as altered gene expression. It will be appreciated that during the course of a disease or condition the expression of different transcripts may vary. Thus at different stages, altered expression may not be exhibited for particular transcripts compared to "normal" samples. However, combining information from several transcripts which exhibit altered expression at one or more stages through the course of the disease or condition can be used to provide a characteristic pattern which is indicative of a particular stage of the disease or condition. Thus for example different stages in cancer, e.g. pre-stage I, stage I, stage II, II or IV can be identified.

"Normal" as used herein refers to organisms or samples which are used for comparative purposes. Preferably, these are "normal" in the sense that they do not exhibit any indication of, or are not believed to have, any disease or condition that would affect gene expression, particularly in respect of the disease for which they are to be used as the normal standard. However, it will be appreciated that different stages of a disease or condition may be compared and in such cases, the "normal" sample may correspond to the earlier stage of the disease or condition.

As used herein a "sample" refers to any material obtained from the organism, e.g. human or non-human animal under investigation which contains cells and includes, tissues, body fluid or body waste or in the case of prokaryotic organisms, the organism itself. "Body fluids" include blood, saliva, spinal fluid, semen, lymph. "Body waste" includes urine, expectorated

matter (pulmonary patients), faeces etc. "Tissue
samples" include tissue obtained by biopsy, by surgical
interventions or by other means e.g. placenta.
Preferably however, the samples which are examined are
5   from areas of the body not apparently affected by the
disease or condition. The cells in such samples are not
disease cells, e.g. cancer cells, have not been in
contact with such disease cells and do not originate
from the site of the disease or condition. The "site of
10   disease" is considered to be that area of the body which
manifests the disease in a way which may be objectively
determined, e.g. a tumour or area of inflammation. Thus
for example peripheral blood may be used for the
diagnosis of non-haematopoietic cancers, and the blood
15   does not require the presence of malignant or
disseminated cells from the cancer in the blood.
Similarly in diseases of the brain, in which no diseased
cells are found in the blood due to the blood:brain
barrier, peripheral blood may still be used in the
20   methods of the invention.

It will however be appreciated that the method of
preparing the standard transcription pattern and other
methods of the invention are also applicable for use on
living parts of eukaryotic organisms such as cell lines
25   and organ cultures and explants.

As used herein, reference to "corresponding" sample
etc. refers to cells preferably from the same tissue,
body fluid or body waste, but also includes cells from
tissue, body fluid or body waste which are sufficiently
30   similar for the purposes of preparing the standard or
test pattern. When used in reference to genes
"corresponding" to the probes, this refers to genes
which are related by sequence (which may be
complementary) to the probes although the probes may
35   reflect different splicing products of expression.

"Assessing" as used herein refers to both
quantitative and qualitative assessment which may be

- 22 -

determined in absolute or relative terms.

The invention may be put into practice as follows.
To prepare a standard transcript pattern for a
particular disease, condition or stage thereof, sample
5   mRNA is extracted from the cells of tissues, body fluid
or body waste according to known techniques (see for
example Sambrook et. al. (1989), Molecular Cloning : A
laboratory manual, 2nd Ed., Cold Spring Harbor
Laboratory Press, Cold Spring Harbor, N.Y.) from a
10   diseased individual or organism.

Owing to the difficulties in working with RNA, the
RNA is preferably reverse transcribed at this stage to
form first strand cDNA. Cloning of the cDNA or
selection from, or using, a cDNA library is not however
15   necessary in this or other methods of the invention.
Preferably, the complementary strands of the first
strand cDNAs are synthesized, ie. second strand cDNAs,
but this will depend on which relative strands are
present in the oligonucleotide probes. The RNA may
20   however alternatively be used directly without reverse
transcription and may be labelled if so required.

Preferably the cDNA strands are amplified by known
amplification techniques such as the polymerase chain
reaction (PCR) by the use of appropriate primers.
25   Alternatively, the cDNA strands may be cloned with a
vector, used to transform a bacteria such as E. coli
which may then be grown to multiply the nucleic acid
molecules. When the sequence of the cDNAs are not
known, primers may be directed to regions of the nucleic
30   acid molecules which have been introduced. Thus for
example, adapters may be ligated to the cDNA molecules
and primers directed to these portions for amplification
of the cDNA molecules. Alternatively, in the case of
eukaryotic samples, advantage may be taken of the polyA
35   tail and cap of the RNA to prepare appropriate primers.

To produce the standard diagnostic gene transcript
pattern or fingerprint for a particular disease or

condition or stage thereof, the above described
oligonucleotide probes are used to probe mRNA or cDNA of
the diseased sample to produce a signal for
hybridization to each particular oligonucleotide probe
5   species, ie. each unique probe. A standard control gene
transcript pattern may also be prepared if desired using
mRNA or cDNA from a normal sample. Thus, mRNA or cDNA
is brought into contact with the oligonucleotide probe
under appropriate conditions to allow hybridization.

10   When multiple samples are probed, this may be
performed consecutively using the same probes, e.g. on
one or more solid supports, ie. on probe kit modules, or
by simultaneously hybridizing to corresponding probes,
e.g. the modules of a corresponding probe kit.

15   To identify when hybridization occurs and obtain an
indication of the number of transcripts/cDNA molecules
which become bound to the oligonucleotide probes, it is
necessary to identify a signal produced when the
transcripts (or related molecules) hybridize (e.g. by
20   detection of double stranded nucleic acid molecules or
detection of the number of molecules which become bound,
after removing unbound molecules, e.g. by washing).

            In order to achieve a signal, either or both
components which hybridize (ie. the probe and the
25   transcript) carry or form a signalling means or a part
thereof. This "signalling means" is any moiety capable
of direct or indirect detection by the generation or
presence of a signal. The signal may be any detectable
physical characteristic such as conferred by radiation
30   emission, scattering or absorption properties, magnetic
properties, or other physical properties such as charge,
size or binding properties of existing molecules (e.g.
labels) or molecules which may be generated (e.g. gas
emission etc.). Techniques are preferred which allow
35   signal amplification, e.g. which produce multiple signal
events from a single active binding site, e.g. by the
catalytic action of enzymes to produce multiple

- 24 -

detectable products.

Conveniently the signalling means may be a label which itself provides a detectable signal. Conveniently this may be achieved by the use of a radioactive or other label which may be incorporated during cDNA production, the preparation of complementary cDNA strands, during amplification of the target mRNA/cDNA or added directly to target nucleic acid molecules.

Appropriate labels are those which directly or indirectly allow detection or measurement of the presence of the transcripts/cDNA. Such labels include for example radiolabels, chemical labels, for example chromophores or fluorophores (e.g. dyes such as fluorescein and rhodamine), or reagents of high electron density such as ferritin, haemocyanin or colloidal gold. Alternatively, the label may be an enzyme, for example peroxidase or alkaline phosphatase, wherein the presence of the enzyme is visualized by its interaction with a suitable entity, for example a substrate. The label may also form part of a signalling pair wherein the other member of the pair is found on, or in close proximity to, the oligonucleotide probe to which the transcript/cDNA binds, for example, a fluorescent compound and a quench fluorescent substrate may be used. A label may also be provided on a different entity, such as an antibody, which recognizes a peptide moiety attached to the transcripts/cDNA, for example attached to a base used during synthesis or amplification.

A signal may be achieved by the introduction of a label before, during or after the hybridization step. Alternatively, the presence of hybridizing transcripts may be identified by other physical properties, such as their absorbance, and in which case the signalling means is the complex itself.

The amount of signal associated with each oligonucleotide probe is then assessed. The assessment may be quantitative or qualitative and may be based on

binding of a single transcript species (or related cDNA
or other products) to each probe, or binding of multiple
transcript species to multiple copies of each unique
probe. It will be appreciated that quantitative results
will provide further information for the transcript
fingerprint of the disease which is compiled. This data
may be expressed as absolute values (in the case of
macroarrays) or may be determined relative to a
particular standard or reference e.g. a normal control
sample.

Furthermore it will be appreciated that the
standard diagnostic gene pattern transcript may be
prepared using one or more disease samples (and normal
samples if used) to perform the hybridization step to
obtain patterns not biased towards a particular
individual's variations in gene expression.

The use of the probes to prepare standard patterns
and the standard diagnostic gene transcript patterns
thus produced for the purpose of identification or
diagnosis or monitoring of a particular disease or
condition or stage thereof in a particular organism
forms a further aspect of the invention.

Once a standard diagnostic fingerprint or pattern
has been determined for a particular disease or
condition using the selected oligonucleotide probes,
this information can be used to identify the presence,
absence or extent or stage of that disease or condition
in a different test organism or individual.

To examine the gene expression pattern of a test
sample, a test sample of tissue, body fluid or body
waste containing cells, corresponding to the sample used
for the preparation of the standard pattern, is obtained
from a patient or the organism to be studied. A test
gene transcript pattern is then prepared as described
hereinbefore as for the standard pattern.

In a further aspect therefore, the present
invention provides a method of preparing a test gene

- 26 -

transcript pattern comprising at least the steps of:

a) isolating mRNA from the cells of a sample of said test organism, which may optionally be reverse transcribed to cDNA;

b) hybridizing the mRNA or cDNA of step (a) to a set of oligonucleotides or a kit as described hereinbefore specific for a disease or condition or stage thereof in an organism and sample thereof corresponding to the organism and sample thereof under investigation; and

c) assessing the amount of mRNA or cDNA hybridizing to each of said probes to produce said pattern reflecting the level of gene expression of genes to which said oligonucleotides bind, in said test sample.

This test pattern may then be compared to one or more standard patterns to assess whether the sample contains cells having the disease, condition or stage thereof.

Thus viewed from a further aspect the present invention provides a method of diagnosing or identifying or monitoring a disease or condition or stage thereof in an organism, comprising the steps of:

a)   isolating mRNA from the cells of a sample of said organism, which may optionally be reverse transcribed to cDNA;

b)   hybridizing the mRNA or cDNA of step (a) to a set of oligonucleotides or a kit as described hereinbefore specific for said disease or condition or stage thereof in an organism and sample thereof corresponding to the organism and sample thereof under investigation;

c)   assessing the amount of mRNA or cDNA hybridizing to each of said probes to produce a characteristic pattern reflecting the level of gene expression of genes to which said oligonucleotides bind, in said sample; and

d)   comparing said pattern to a standard

diagnostic pattern prepared according to the method of the invention using a sample from an organism corresponding to the organism and sample under investigation to determine the presence of said disease or condition or a stage thereof in the organism under investigation.

The method up to and including step c) is the preparation of a test pattern as described above.

As referred to herein, "diagnosis" refers to determination of the presence or existence of a disease or condition or stage thereof in an organism. "Monitoring" refers to establishing the extent of a disease or condition, particularly when an individual is known to be suffering from a disease or condition, for example to monitor the effects of treatment or the development of a disease or condition, e.g. to determine the suitability of a treatment or provide a prognosis.

The presence of the disease or condition or stage thereof may be determined by determining the degree of correlation between the standard and test samples' patterns. This necessarily takes into account the range of values which are obtained for normal and diseased samples. Although this can be established by obtaining standard deviations for several representative samples binding to the probes to develop the standard, it will be appreciated that single samples may be sufficient to generate the standard pattern to identify a disease if the test sample exhibits close enough correlation to that standard. Conveniently, the presence, absence, or extent of a disease or condition or stage thereof in a test sample can be predicted by inserting the data relating to the expression level of informative probes in test sample into the standard diagnostic probe pattern established according to equation 1.

Data generated using the above mentioned methods may be analysed using various techniques from the most

- 28 -

basic visual representation (e.g. relating to intensity) to more complex data manipulation to identify underlying patterns which reflect the interrelationship of the level of expression of each gene to which the various probes bind, which may be quantified and expressed mathematically. Conveniently, the raw data thus generated may be manipulated by the data processing and statistical methods described hereinafter, particularly normalizing and standardizing the data and fitting the data to a classification model to determine whether said test data reflects the pattern of a particular disease, condition or stage thereof.

The methods described herein may be used to identify, monitor or diagnose a disease, condition or ailment or its stage or progression, for which the oligonucleotide probes are informative. "Informative" probes as described herein, are those which reflect genes which have altered expression in the diseases or conditions in question, or particular stages thereof. Probes of the invention may not be sufficiently informative for diagnostic purposes when used alone, but are informative when used as one of several probes to provide a characteristic pattern, e.g. in a set as described hereinbefore.

Preferably said probes correspond to genes which are systemically affected by said disease, condition or stage thereof. Especially preferably said genes, from which transcripts are derived which bind to probes of the invention, are metabolic or house-keeping genes and preferably are moderately or highly expressed. The advantage of using probes directed to moderately or highly expressed genes is that smaller clinical samples are required for generating the necessary gene expression data set, e.g. less than 1ml blood samples.

Furthermore, it has been found that such genes which are already being actively transcribed tend to be more prone to being influenced, in a positive or

- 29 -

negative way, by new stimuli. In addition, since
transcripts are already being produced at levels which
are generally detectable, small changes in those levels
are readily detectable as for example, a certain
5   detectable threshold does not need to be reached.

In preferred methods of the invention, the set of
probes of the invention are informative for a variety of
different diseases, conditions or stages thereof. A
sub-set of the probes disclosed herein may be used for
10   diagnosis, identification or monitoring a particular
disease, condition or stage thereof.

Thus the probes may be used to diagnose or identify
or monitor any condition, ailment, disease or reaction
that leads to the relative increase or decrease in the
15   activity of informative genes of any or all eukaryotic
or prokaryotic organisms regardless of whether these
changes have been caused by the influence of bacteria,
virus, prions, parasites, fungi, radiation, natural or
artificial toxins, drugs or allergens, including mental
20   conditions due to stress, neurosis, psychosis or
deteriorations due to the ageing of the organism, and
conditions or diseases of unknown cause, providing a
sub-set of the probes as described herein are
informative for said disease or condition or stage
25   thereof.

Such diseases include those which result in
metabolic or physiological changes, such as fever-
associated diseases such as influenza or malaria. Other
diseases which may be detected include for example
30   yellow fever, sexually transmitted diseases such as
gonorrhea, fibromyalgia, candida-related complex, cancer
(for example of the stomach, lung, breast, prostate
gland, bowel, skin, colon, ovary etc), Alzheimer's
disease, disease caused by retroviruses such as HIV,
35   senile dementia, multiple sclerosis and Creutzfeldt-
Jakob disease to mention a few.

The invention may also be used to identify patients

- 30 -

with psychiatric or psychosomatic diseases such as schizophrenia and eating disorders. Of particular importance is the use of this method to detect diseases, conditions, or stages thereof, which are not readily detectable by known diagnostic methods, such as HIV which is generally not detectable using known techniques 1 to 4 months following infection. Conditions which may be identified include for example drug abuse, such as the use of narcotics, alcohol, steroids or performance enhancing drugs.

Preferably said disease to be identified or monitored is a cancer or a degenerative brain disorder (such as Alzheimer's or Parkinson's disease).

In particular, a set of oligonucleotide probes, wherein said set comprises at least 10 oligonucleotides selected from:

an oligonucleotide as described in Table 4 or an oligonucleotide derived therefrom or an oligonucleotide with a complementary sequence, or a functionally equivalent oligonucleotide,

may be used for diagnosis or identification or monitoring the progression of Alzheimer's disease. Similarly Table 2 probes and Table 2 derived probes and their functional equivalents may be used to diagnose, identify or monitor the progression of breast cancer. Especially preferably the probes used for breast cancer analysis are selected based on their occurrence as set forth in Table 3 and as described hereinbefore.

The diagnostic method may be used alone as an alternative to other diagnostic techniques or in addition to such techniques. For example, methods of the invention may be used as an alternative or additive diagnostic measure to diagnosis using imaging techniques such as Magnetic Resonance Imagine (MRI), ultrasound imaging, nuclear imaging or X-ray imaging, for example in the identification and/or diagnosis of tumours.

The methods of the invention may be performed on

- 31 -

cells from prokaryotic or eukaryotic organisms which may
be any eukaryotic organisms such as human beings, other
mammals and animals, birds, insects, fish and plants,
and any prokaryotic organism such as a bacteria.

5   Preferred non-human animals on which the methods of
the invention may be conducted include, but are not
limited to mammals, particularly primates, domestic
animals, livestock and laboratory animals. Thus
preferred animals for diagnosis include mice, rats,
10   guinea pigs, cats, dogs, pigs, cows, goats, sheep,
horses. Particularly preferably the disease state or
condition of humans is diagnosed, identified or
monitored.

          As described above, the sample under study may be
15   any convenient sample which may be obtained from an
organism. Preferably however, as mentioned above, the
sample is obtained from a site distant to the site of
disease and the cells in such samples are not disease
cells, have not been in contact with such cells and do
20   not originate from the site of the disease or condition.
In such cases, although preferably absent, the sample
may contain cells which do not fulfil these criteria.
However, since the probes of the invention are concerned
with transcripts whose expression is altered in cells
25   which do satisfy these criteria, the probes are
specifically directed to detecting changes in transcript
levels in those cells even if in the presence of other,
background cells.

          It has been found that the cells from such samples
30   show significant and informative variations in the gene
expression of a large number of genes. Thus, the same
probe (or several probes) may be found to be informative
in determinations regarding two or more diseases,
conditions or stages thereof by virtue of the particular
35   level of transcripts binding to that probe or the
interrelationship of the extent of binding to that probe
relative to other probes. As a consequence, it is

- 32 -

possible to use a relatively small number of probes for
screening for multiple disorders or diseases. This has
consequences with regard to the selection of probes,
discussed in relation to random identification of probes
5   hereinafter, but also for the use of a single set of
probes for more than one diagnosis. Table 9 which
represents preferred probes of the invention discloses
probes which are informative for both Alzheimer's and
breast cancer.

10   Thus, the present invention also provides sets of
probes for diagnosing, identifying or monitoring two or
more diseases, conditions or stages thereof, wherein at
least one of said probes is suitable for said
diagnosing, identifying or monitoring at least two of
15   said diseases, conditions or stages thereof, and kits
and methods of using the same. Preferably at least 5
probes, e.g. from 5 to 15 probes, are used in at least
two diagnoses.

         Thus, in a further preferred aspect, the present
20   invention provides a method of diagnosis or
identification or monitoring as described hereinbefore
for the diagnosis, identification or monitoring of two
or more diseases, conditions or stages thereof in an
organism, wherein said test pattern produced in step c)
25   of the diagnostic method is compared in step d) to at
least two standard diagnostic patterns prepared as
described previously, wherein each standard diagnostic
pattern is a pattern generated for a different disease
or condition or stage thereof.

30   Whilst in a preferred aspect the methods of
assessment concern the development of a gene transcript
pattern from a test sample and comparison of the same to
a standard pattern, the elevation or depression of
expression of certain markers may also be examined by
35   examining the products of expression and the level of
those products. Thus a standard pattern in relation to
the expressed product may be generated:

- 33 -

In such methods the levels of expression of a set of polypeptides encoded by the gene to which an oligonucleotide of Table 1 or a Table 1 derived oligonucleotide, binds, are analysed.

Various diagnostic methods may be used to assess the amount of polypeptides (or fragments thereof) which are present. The presence or concentration of polypeptides may be examined, for example by the use of a binding partner to said polypeptide (e.g. an antibody), which may be immobilized, to separate said polypeptide from the sample and the amount of polypeptide may then be determined.

"Fragments" of the polypeptides refers to a domain or region of said polypeptide, e.g. an antigenic fragment, which is recognizable as being derived from said polypeptide to allow binding of a specific binding partner. Preferably such a fragment comprises a significant portion of said polypeptide and corresponds to a product of normal post-synthesis processing.

Thus in a further aspect the present invention provides a method of preparing a standard gene transcript pattern characteristic of a disease or condition or stage thereof in an organism comprising at least the steps of:

a) releasing target polypeptides from a sample of one or more organisms having the disease or condition or stage thereof;

b) contacting said target polypeptides with one or more binding partners, wherein each binding partner is specific to a marker polypeptide (or a fragment thereof) encoded by the gene to which an oligonucleotide of Table 1 (or derived from a sequence described in Table 1) binds, to allow binding of said binding partners to said target polypeptides, wherein said marker polypeptides are specific for said disease or condition thereof in an organism and sample thereof corresponding to the organism and sample thereof under investigation; and

- 34 -

c) assessing the target polypeptide binding to said
binding partners to produce a characteristic pattern
reflecting the level of gene expression of genes which
express said marker polypeptides, in the sample with the
disease, condition or stage thereof.

As used herein "target polypeptides" refer to those
polypeptides present in a sample which are to be
detected and "marker polypeptides" are polypeptides
which are encoded by the genes to which Table 1
oligonucleotides or Table 1 derived oligonucleotides
bind. The target and marker polypeptides are identical
or at least have areas of high similarity, e.g. epitopic
regions to allow recognition and binding of the binding
partner.

"Release" of the target polypeptides refers to
appropriate treatment of a sample to provide the
polypeptides in a form accessible for binding of the
binding partners, e.g. by lysis of cells where these are
present. The samples used in this case need not
necessarily comprise cells as the target polypeptides
may be released from cells into the surrounding tissue
or fluid, and this tissue or fluid may be analysed, e.g.
urine or blood. Preferably however the preferred
samples as described herein are used. "Binding
partners" comprise the separate entities which together
make an affinity binding pair as described above,
wherein one partner of the binding pair is the target or
marker polypeptide and the other partner binds
specifically to that polypeptide, e.g. an antibody.

Various arrangements may be envisaged for detecting
the amount of binding pairs which form. In its simplest
form, a sandwich type assay e.g. an immunoassay such as
an ELISA, may be used in which an antibody specific to
the polypeptide and carrying a label (as described
elsewhere herein) may be bound to the binding pair (e.g.
the first antibody:polypeptide pair) and the amount of
label detected.

- 35 -

Other methods as described herein may be similarly modified for analysis of the protein product of expression rather than the gene transcript and related nucleic acid molecules.

Thus a further aspect of the invention provides a method of preparing a test gene transcript pattern comprising at least the steps of:

a) releasing target polypeptides from a sample of said test organism;

b) contacting said target polypeptides with one or more binding partners, wherein each binding partner is specific to a marker polypeptide (or a fragment thereof) encoded by the gene to which an oligonucleotide of Table 1 (or derived from a sequence described in Table 1) binds, to allow binding of said binding partners to said target polypeptides, wherein said marker polypeptides are specific for said disease or condition thereof in an organism and sample thereof corresponding to the organism and sample thereof under investigation; and

c) assessing the target polypeptide binding to said binding partners to produce a characteristic pattern reflecting the level of gene expression of genes which express said marker polypeptides, in said test sample.

A yet further aspect of the invention provides a method of diagnosing or identifying or monitoring a disease or condition or stage thereof in an organism comprising the steps of:

a) releasing target polypeptides from a sample of said organism;

b) contacting said target polypeptides with one or more binding partners, wherein each binding partner is specific to a marker polypeptide (or a fragment thereof) encoded by the gene to which an oligonucleotide of Table 1 (or derived from a sequence described in Table 1) binds, to allow binding of said binding partners to said target polypeptides, wherein said marker polypeptides are specific for said disease or condition thereof in an

organism and sample thereof corresponding to the
organism and sample thereof under investigation; and
    c) assessing the target polypeptide binding to said
binding partners to produce a characteristic pattern
reflecting the level of gene expression of genes which
express said marker polypeptides in said sample; and
    d) comparing said pattern to a standard diagnostic
pattern prepared as described hereinbefore using a
sample from an organism corresponding to the organism
and sample under investigation to determine the degree
of correlation indicative of the presence of said
disease or condition or a stage thereof in the organism
under investigation.

    The methods of generating standard and test
patterns and diagnostic techniques rely on the use of
informative oligonucleotide probes to generate the gene
expression data. In some cases it will be necessary to
select these informative probes for a particular method,
e.g. to diagnose a particular disease, from a selection
of available probes, e.g. the probes described
hereinbefore (the Table 1 oligonucleotides, the Table 1
derived oligonucleotides, their complementary sequences
and functionally equivalent oligonucleotides). The
following methodology describes a convenient method for
identifying such informative probes, or more
particularly how to select a suitable sub-set of probes
from the probes described herein.

    Probes for the analysis of a particular disease or
condition or stage thereof, may be identified in a
number of ways known in the prior art, including by
differential expression or by library subtraction (see
for example WO98/49342). As described hereinafter, in
view of the high information content of most
transcripts, as a starting point one may also simply
analyse a random sub-set of mRNA or cDNA species and
pick the most informative probes from that sub-set. The
following method describes the use of immobilized

- 37 -

oligonucleotide probes (e.g. the probes of the
invention) to which mRNA (or related molecules) from
different samples is bound to identify which probes are
the most informative to identify a particular type of
5   sample, e.g. a disease sample.

The immobilized probes can be derived from various
unrelated or related organisms; the only requirement is
that the immobilized probes should bind specifically to
their homologous counterparts in test organisms. Probes
10   can also be derived from commercially available or
public databases and immobilized on solid supports or,
as mentioned above, they can be randomly picked and
isolated from a cDNA library and immobilized on a solid
support.

15   The length of the probes immobilised on the solid
support should be long enough to allow for specific
binding to the target sequences. The immobilised probes
can be in the form of DNA, RNA or their modified
products or PNAs (peptide nucleic acids). Preferably,
20   the probes immobilised should bind specifically to their
homologous counterparts representing highly and
moderately expressed genes in test organisms.
Conveniently the probes which are used are the probes
described herein.

25   The gene expression pattern of cells in biological
samples can be generated using prior art techniques such
as microarray or macroarray as described below or using
methods described herein. Several technologies have now
been developed for monitoring the expression level of a
30   large number of genes simultaneously in biological
samples, such as, high-density oligoarrays (Lockhart et
al., 1996, Nat. Biotech., 14, p1675-1680), cDNA
microarrays (Schena et al, 1995, Science, 270, p467-470)
and cDNA macroarrays (Maier E et al., 1994, Nucl. Acids
35   Res., 22, p3423-3424; Bernard et al., 1996, Nucl. Acids
Res., 24, p1435-1442).

In high-density oligoarrays and cDNA microarrays,

- 38 -

hundreds and thousands of probe oligonucleotides or
cDNAs, are spotted onto glass slides or nylon membranes,
or synthesized on biochips. The mRNA isolated from the
test and reference samples are labelled by reverse
5   transcription with a red or green fluorescent dye,
mixed, and hybridised to the microarray. After washing,
the bound fluorescent dyes are detected by a laser,
producing two images, one for each dye. The resulting
ratio of the red and green spots on the two images
10   provides the information about the changes in expression
levels of genes in the test and reference samples.
Alternatively, single channel or multiple channel
microarray studies can also be performed.

       In cDNA macroarray, different cDNAs are spotted on
15   a solid support such as nylon membranes in excess in
relation to the amount of test mRNA that can hybridise
to each spot. mRNA isolated from test samples is radio-
labelled by reverse transcription and hybridised to the
immobilised probe cDNA. After washing, the signals
20   associated with labels hybridising specifically to
immobilised probe cDNA are detected and quantified. The
data obtained in macroarray contains information about
the relative levels of transcripts present in the test
samples. Whilst macroarrays are only suitable to
25   monitor the expression of a limited number of genes,
microarrays can be used to monitor the expression of
several thousand genes simultaneously and is, therefore,
a preferred choice for large-scale gene expression
studies.

30   A macroarray technique for generating the gene
expression data set has been used to illustrate the
probe identification method described herein. For this
purpose, mRNA is isolated from samples of interest and
used to prepare labelled target molecules, e.g. mRNA or
35   cDNA as described above. The labelled target molecules
are then hybridised to probes immobilised on the solid
support. Various solid supports can be used for the

purpose, as described previously. Following
hybridization, unbound target molecules are removed and
signals from target molecules hybridizing to immobilised
probes quantified. If radio labelling is performed,
PhosphoImager can be used to generate an image file that
can be used to generate a raw data set. Depending on
the nature of label chosen for labelling the target
molecules, other instruments can also be used, for
example, when fluorescence is used for labelling, a
FluoroImager can be used to generate an image file from
the hybridised target molecules.

The raw data corresponding to mean intensity,
median intensity, or volume of the signals in each spot
can be acquired from the image file using commercially
available software for image analysis. However, the
acquired data needs to be corrected for background
signals and normalized prior to analysis, since, several
factors can affect the quality and quantity of the
hybridising signals. For example, variations in the
quality and quantity of mRNA isolated from sample to
sample, subtle variations in the efficiency of labelling
target molecules during each reaction, and variations in
the amount of unspecific binding between different
macroarrays can all contribute to noise in the acquired
data set that must be corrected for prior to analysis.

Background correction can be performed in several
ways. The lowest pixel intensity within a spot can be
used for background subtraction or the mean or median of
the line of pixels around the spots' outline can be used
for the purpose. One can also define an area
representing the background intensity based on the
signals generated from negative controls and use the
average intensity of this area for background
subtraction.

The background corrected data can then be
transformed for stabilizing the variance in the data
structure and normalized for the differences in probe

intensity.   Several transformation techniques have been
described in the literature and a brief overview can be
found in Cui, Kerr and Churchill
http://www.jax.org/research/churchill/research/
5   expression/Cui-Transform.pdf).   Normalization can be
performed by dividing the intensity of each spot with
the collective intensity, average intensity or median
intensity of all the spots in a macroarray or a group of
spots in a macroarray in order to obtain the relative
10   intensity of signals hybridising to immobilised probes
in a macroarray.   Several methods have been described
for normalizing gene expression data (Richmond and
Somerville, 2000, Current Opin. Plant Biol., 3, p108-
116; Finkelstein et al., 2001, In "Methods of Microarray
15   Data Analysis.   Papers from CAMDA, Eds. Lin & Johnsom,
Kluwer Academic, p57-68; Yang et al., 2001, In "Optical
Technologies and Informatics", Eds. Bittner, Chen,
Dorsel & Dougherty, Proceedings of SPIE, 4266, p141-152;
Dudoit et al, 2000, J. Am. Stat. Ass., 97, p77-87; Alter
20   et al 2000, supra; Newton et al., 2001, J. Comp. Biol.,
8, p37-52).   Generally, a scaling factor or function is
first calculated to correct the intensity effect and
then used for normalising the intensities. The use of
external controls has also been suggested for improved
25   normalization.

One other major challenge encountered in
large-scale gene expression analysis is that of
standardization of data collected from experiments
performed at different times.   We have observed that
30   gene expression data for samples acquired in the same
experiment can be efficiently compared following
background correction and normalization.   However, the
data from samples acquired in experiments performed at
different times requires further standardization prior
35   to analysis.   This is because subtle differences in
experimental parameters between different experiments,
for example, differences in the quality and quantity of

mRNA extracted at different times, differences in time used for target molecule labelling, hybridization time or exposure time, can affect the measured values. Also, factors such as the nature of the sequence of

5   transcripts under investigation (their GC content) and their amount in relation to the each other determines how they are affected by subtle variations in the experimental processes. They determine, for example, how efficiently first strand cDNAs, corresponding to a

10   particular transcript, are transcribed and labelled during first strand synthesis, or how efficiently the corresponding labelled target molecules bind to their complementary sequences during hybridization. Batch to batch difference in the printing process is also a major

15   factor for variation in the generated expression data.

Failure to properly address and rectify for these influences leads to situations where the differences between the experimental series may overshadow the main information of interest contained in the gene expression

20   data set, i.e. the differences within the combined data from the different experimental series. Figure 1 provides one such example showing a classification based on Principal Component Analysis (PCA) of combined data from two experimental series where the main goal is to

25   distinguish between Alzheimer/non-Alzheimer patients.

PCA (also known as singular value decomposition) is a technique for studying interdependencies and underlying relationships of a set of variables. The data are modelled in terms of a few significant factors

30   or principal components (PC's), plus residuals. The PC's contain the main phenomena and define the systematic variability present in the data, while the residuals represent the variability interpreted as noise. Details on PCA can be found in Jollife (1986,

35   Principal Component Analysis, Springer-Verlag, NY), and Jackson (1991, A User's Guide to Principal Components, Wiley, NY). The results of Figure 1 show that two

clusters are formed representing the data from two
experimental series rather than the
Alzheimer/non-Alzheimer differentiation. There were
eight samples in common between the two series of

5   experiments, which ideally should have fallen on top of,
or in near proximity to, each other if appropriately
standardized.

     We have now found that gene expression data between
different experiments can be efficiently standardized by

10   including a subset of samples from one experimental
series in the next experimental series and using a
direct standardization method (DS), originally described
by Wang and Kowalski (Anal. Chem., 1991, 63, p2750 and
J. Chemometrics, 1991, 5, p129-145). Although the

15   method of DS is well known in the field of analytical
chemistry, it remains undescribed and unused in the
field of gene expression data analysis.

     In DS, the secondary data representing for example
experimental series 2 (secondary measurements, R_2) are

20   corrected to match the data measured on the primary
measurements representing data from series 1 (R_1), while
the calibration model remains unchanged. In DS,
response matrices for both experimental series are
related to each other by a transformation matrix F, i.e.

25

$$R_1 = R_2 F \qquad (1)$$

     Where F is a square matrix dimensioned gene by
gene. From (1), the transformation matrix is calculated
as:

30

$$F = R_2^+ R_1 \qquad (2)$$

     The transformation matrix F in equation (2) is
calculated using a relatively small subset of samples
which are measured on both the master primary and the

35   secondary series of data.

     Finally, the response of the unknown sample
measured on the secondary series $r^T_{2,un}$, is standardized

- 43 -

to the response vector $\hat{r}^T_{1,un}$ expected from the primary series

$$\hat{r}^T_{1,un} = rT_{21,un}\hat{F} \qquad (3)$$

From the preceding equation it can be seen that the column i of the transformation matrix contains the multiplication factors for a set of genes measured in the secondary series to obtain the intensity at spot i of the corrected series.

The number of samples that are repeated in the experimental series, R_1 and R_2, should be equal to their ranks, which in this case is equal to the number of principal components retained for explaining the variation in the R_1 and R_2. For example, if three principal components are retained for explaining the variation in the data set, a minimum of three samples should be repeated between R_1 and R_2. The samples that should be repeated between different series should ideally be those that exhibit high leverages in the gene expression pattern. At times, two samples may suffice, while at other times, more than two samples should be ideally be included for good representativity. In some cases, the samples selected can be the same in all the experimental series to be compared (reference samples), while in other cases, representative samples can be selected sequentially by analyzing the expression pattern after each experiment. The selected samples with high leverages are then included in the next experimental series. The results of using Direct Standardization are shown in Figure 1.

Another approach for normalizing and standardizing the gene expression data set is to hybridize each DNA array with target molecules prepared from a test sample and an equal amount of labelled target molecules prepared from representative reference samples. In order to measure the intensity of labelled target

molecules hybridizing to the immobilized probes it is
necessary that the labelled molecules are prepared from
test and reference samples using different labels, for
example, different fluorescent dyes can be used for
preparing the labelled material. The labelled molecules
prepared from reference samples can be added to the
hybridization solution together with the labelled
material prepared from test samples. A data file from
each array representing the expression pattern of
different genes in the test sample and reference samples
can then be obtained, normalized and standardized by the
direct standardization method as described above. An
instant advantage of including the differentially
labelled target molecules from reference samples during
hybridization is that it enables an efficient comparison
of new test samples to the data sets already stored in a
database.

Monitoring the expression of a large number of
genes in several samples leads to the generation of a
large amount of data that is too complex to be easily
interpreted. Several unsupervised and supervised
multivariate data analysis techniques have already been
shown to be useful in extracting meaningful biological
information from these large data sets. Cluster
analysis is by far the most commonly used technique for
gene expression analysis, and has been performed to
identify genes that are regulated in a similar manner,
and or identifying new/unknown tumour classes using gene
expression profiles (Eisen et al., 1998, PNAS, 95,
p14863-14868, Alizadeh et al. 2000, supra, Perou et al.
2000, Nature, 406, p747-752; Ross et al, 2000, Nature
Genetics, 24(3), p227-235; Herwig et al., 1999, Genome
Res., 9, p1093-1105; Tamayo et al, 1999, Science, PNAS,
96, p2907-2912).

In the clustering method, genes are grouped into
functional categories (clusters) based on their
expression profile, satisfying two criteria: *homogeneity*

- the genes in the same cluster are highly similar in expression to each other; and *separation* - genes in different clusters have low similarity in expression to each other.

Examples of various clustering techniques that have been used for gene expression analysis include hierarchical clustering (Eisen et al., 1998, supra; Alizadeh et al. 2000, supra; Perou et al. 2000, supra; Ross et al, 2000, supra), K-means clustering (Herwig et al., 1999, supra; Tavazoie et al, 1999, Nature Genetics, 22(3), p. 281-285), gene shaving (Hastie et al., 2000, Genome Biology, 1(2), research 0003.1-0003.21), block clustering (Tibshirani et al., 1999, Tech repot Univ Stanford.) Plaid model (Lazzeroni, 2002, Stat. Sinica, 12, p61-86), and self-organizing maps (Tamayo et al. 1999, supra). Also, related methods of multivariate statistical analysis, such as those using the singular value decomposition (Alter et al., 2000, PNAS, 97(18), p10101-10106; Ross et al. 2000, supra) or multidimensional scaling can be effective at reducing the dimensions of the objects under study.

However, methods such as cluster analysis and singular value decomposition are purely exploratory and only provide a broad overview of the internal structure present in the data. They are unsupervised approaches in which the available information concerning the nature of the class under investigation is not used in the analysis. Often, the nature of the biological perturbation to which a particular sample has been subjected is known. For example, it is sometimes known whether the sample whose gene expression pattern is being analysed derives from a diseased or healthy individual. In such instances, discriminant analysis can be used for classifying samples into various groups based on their gene expression data.

In such an analysis one builds the classifier by training the data that is capable of discriminating

- 46 -

between member and non-members of a given class. The
trained classifier can then be used to predict the class
of unknown samples. Examples of discrimination methods
that have been described in the literature include
Support Vector Machines (Brown et al, 2000, PNAS, 97,
p262-267), Nearest Neighbour (Dudoit et al., 2000,
supra), Classification trees (Dudoit et al., 2000,
supra), Voted classification (Dudoit et al., 2000,
supra), Weighted Gene voting (Golub et al. 1999, supra),
and Bayesian classification (Keller et al. 2000, Tec
report Univ of Washington). Also a technique in which
PLS (Partial Least Square) regression analysis is first
used to reduce the dimensions in the gene expression
data set followed by classification using logistic
discriminant analysis and quadratic discriminant
analysis (LD and QDA) has recently been described
(Nguyen & Rocke, 2002, Bioinformatics, 18, p39-50 and
1216-1226).

A challenge that gene expression data poses to
classical discriminatory methods is that the number of
genes whose expression are being analysed is very large
compared to the number of samples being analysed.
However in most cases only a small fraction of these
genes are informative in discriminant analysis problems.
Moreover, there is a danger that the noise from
irrelevant genes can mask or distort the information
from the informative genes. Several methods have been
suggested in literature to identify and select genes
that are informative in microarray studies, for example,
t-statistics (Dudoit et al, 2002, J. Am. Stat. Ass., 97,
p77-87), analysis of variance (Kerr et al., 2000, PNAS,
98, p8961-8965), Neighbourhood analysis (Golub et al,
1999, supra), Ratio of between groups to within groups
sum of squares (Dudoit et al., 2002, supra), Non
parametric scoring (Park et al., 2002, Pacific Symposium
on Biocomputing, p52-63) and Likelihood selection
(Keller et al., 2000, supra).

- 47 -

In the methods described herein the gene expression
data that has been normalized and standardized is
analysed by using Partial Least Squares Regression
(PLSR). Although PLSR is primarily a method used for
5   regression analysis of continuous data (see Appendix A),
it can also be utilized as a method for model building
and discriminant analysis using a dummy response matrix
based on a binary coding. The class assignment is based
on a simple dichotomous distinction such as breast
10   cancer (class 1) / healthy (class 2), or a multiple
distinction based on multiple disease diagnosis such as
breast cancer (class 1) / Alzheimer (class 2) / healthy
(class 3). The list of diseases for classification can
be increased depending upon the samples available
15   corresponding to other diseases or conditions or stages
thereof.

PLSR applied as a classification method is referred
to as PLS-DA (DA standing for Discriminant analysis).
PLS-DA is an extension of the PLSR algorithm in which
20   the Y-matrix is a dummy matrix containing n rows
(corresponding to the number of samples) and K columns
(corresponding to the number of classes). The Y-matrix
is constructed by inserting 1 in the kth column and -1
in all the other columns if the corresponding ith object
25   of X belongs to class k. By regressing Y onto X,
classification of a new sample is achieved by selecting
the group corresponding to the largest component of the
fitted, $\hat{y}(x) = (\hat{y}_1(x), \hat{y}_2(x), \ldots, \hat{y}_k(x))$. Thus, in a
-1/1 response matrix, a prediction value below 0 means
30   that the sample belongs to the class designated as -1,
while a prediction value above 0 implies that the sample
belongs to the class designated as 1.

An advantage of PLSR-DA is that the results
obtained can be easily represented in the form of two
35   different plots, the score and loading plots. Score
plots represent a projection of the samples onto the
principal components and shows the distribution of the

- 48 -

samples in the classification model and their
relationship to one another. Loading plots display
correlations between the variables present in the data
set.

5   It is usually recommended to use PLS-DA as a
starting point for the classification problem due to its
ability to handle collinear data, and the property of
PLSR as a dimension reduction technique. Once this
purpose has been satisfied, it is possible to use other

10   methods such as Linear discriminant analysis, LDA, that
has been shown to be effective in extracting further
information, Indahl et al. (1999, Chem. and Intell. Lab.
Syst., 49, p19-31). This approach is based on first
decomposing the data using PLS-DA, and then using the

15   scores vectors (instead of the original variables) as
input to LDA. Further details on LDA can be found in
Duda and Hart (Classification and Scene Analysis, 1973,
Wiley, USA).

       The next step following model building is of model

20   validation. This step is considered to be amongst the
most important aspects of multivariate analysis, and
tests the "goodness" of the calibration model which has
been built. In this work, a cross validation approach
has been used for validation. In this approach, one or

25   a few samples are kept out in each segment while the
model is built using a full cross-validation on the
basis of the remaining data. The samples left out are
then used for prediction/classification. Repeating the
simple cross-validation process several times holding

30   different samples out for each cross-validation leads to
a so-called double cross-validation procedure. This
approach has been shown to work well with a limited
amount of data, as is the case in some of the Examples
described here. Also, since the cross validation step

35   is repeated several times the dangers of model bias and
overfitting are reduced.

       Once a calibration model has been built and

- 49 -

validated, genes exhibiting an expression pattern that is most relevant for describing the desired information in the model can be selected by techniques described in the prior art for variable selection, as mentioned elsewhere. Variable selection will help in reducing the final model complexity, provide a parsimonious model, and thus lead to a reliable model that can be used for prediction. Moreover, use of fewer genes for the purpose of providing diagnosis will reduce the cost of the diagnostic product. In this way informative probes which would bind to the genes of relevance may be identified.

We have found that after a calibration model has been built, statistical techniques like Jackknife (Effron, 1982, The Jackknife, the Bootstrap and other resampling plans. Society for Industrial and Applied mathematics, Philadelphia, USA), based on resampling methodology, can be efficiently used to select or confirm significant variables (informative probes).

The approximate uncertainty variance of the PLS regression coefficients B can be estimated by:

$$S^2B = \sum_{m=1}^{M} ((B-B_m)g)^2$$

where
S^2B = estimated uncertainty variance of B;
B = the regression coefficient at the cross validated rank A using all the N objects;
B_m = the regression coefficient at the rank A using all objects except the object(s) left out in cross validation segment m; and
g = scaling coefficient (here: g=1).

In our approach, Jackknife has been implemented together with cross-validation. For each variable the difference between the B-coefficients B_i in a

- 50 -

cross-validated sub-model and B_{tot} for the total model is
first calculated. The sum of the squares of the
differences is then calculated in all sub-models to
obtain an expression of the variance of the B_i estimate
for a variable. The significance of the estimate of B_i
is calculated using the t-test. Thus, the resulting
regression coefficients can be presented with
uncertainty limits that correspond to 2 Standard
Deviations, and from that significant variables are
detected.

No further details as to the implementation or use
of this step are provided here since this has been
implemented in commercially available software, The
Unscrambler, CAMO ASA, Norway. Also, details on
variable selection using Jackknife can be found in
Westad & Martens (2000, J. Near Inf. Spectr., 8, p117-
124).

The following approach can be used to select
informative probes from a gene expression data set:
    a)   keep out one unique sample (including its
repetitions if present in the data set) per cross
validation segment;
    b)   build a calibration model (cross validated
segment) on the remaining samples using PLSR-DA;
    c)   select the significant genes for the model in
step b) using the Jackknife criterion;
    d)   repeat the above 3 steps until all the unique
samples in the data set are kept out once (as described
in step a). For example, if 75 unique samples are
present in the data set, 75 different calibration models
are built resulting in a collection of 75 different sets
of significant probes;
    e)   select the most significant variables using
the frequency of occurrence criterion in the generated
sets of significant probes in step d). For example, a
set of probes appearing in all sets (100%) are more
informative than probes appearing in only 50% of the

generated sets in step d).

Once the informative probes for a disease have been
selected, a final model is made and validated. The two
most commonly used ways of validating the model are
5   cross-validation (CV) and test set validation. In
cross-validation, the data is divided into k subsets.
The model is then trained k times, each time leaving out
one of the subsets from training, but using only the
omitted subset to compute error criterion, RMSEP (Root
10   Mean Square Error of Prediction). If k equals the
sample size, this is called "leave-one-out" cross-
validation. The idea of leaving one or a few samples
out per validation segment is valid only in cases where
the covariance between the various experiments is zero.
15   Thus, one sample at-a-time approach can not be justified
in situations containing replicates since keeping only
one of the replicates out will introduce a systematic
bias in our analysis. The correct approach in this case
will be to leave out all replicates of the same samples
20   at a time since that would satisfy assumptions of zero
covariance between the CV-segments.

The second approach for model validation is to use
a separate test-set for validating the calibration
model. This requires running a separate set of
25   experiments to be used as a test set. This is the
preferred approach given that real test data are
available.

The final model is then used to identify a disease,
condition or stage thereof in test samples. For this
30   purpose, expression data of selected informative genes
is generated from test samples and then the final model
is used to determine whether a sample belongs to a
diseased or non-diseased class or has a condition or
stage thereof.

35   Thus viewed from a yet further aspect the present
invention provides a method of identifying probes useful
for diagnosing or identifying or monitoring a disease or

- 52 -

condition or stage thereof in an organism, comprising
the steps of:

      a)   immobilizing a set of oligonucleotide probes,
preferably as described hereinbefore, on a

5   solid support;

      b)   isolating mRNA from a sample of a normal
organism (normal sample), which may optionally
be reverse transcribed to cDNA;

      c)   isolating mRNA from a sample from an organism,

10   corresponding to the sample and organism of
step (b), which is known to have said disease
or condition or a stage thereof (diseased
sample), which may optionally be reverse
transcribed to cDNA;

15   d)   hybridizing the mRNA or cDNA of steps (b) and
(c) to said set of immobilized oligonucleotide
probes of step (a); and

      e)   assessing the amount of mRNA or cDNA
hybridizing to each of said oligonucleotide

20   probes to determine the level of gene
expression of genes to which said
oligonucleotide probes bind in said normal and
diseased samples to generate a gene expression
data set for each sample;

25   f)   normalizing and standardizing said data set of
step (e);

      g)   constructing a calibration model for
classification, preferably using the
statistical techniques Partial Least Squares

30   Discriminant Analysis (PLS-DA) and Linear
Discriminant Analysis (LDA);

      h)   performing JackKnife analysis and identifying
those oligonucleotide probes which are
required for classification of said disease

35   and normal samples into their respective
groups.

Preferably a model for classification purposes is

- 53 -

generated by using the data relating to the probes
identified according to the above described method.
Preferably the sample is as described previously.
Preferably the oligonucleotides which are immobilized in
5   step (a) are randomly selected as described below or are
the probes as described hereinbefore. Such
oligonucleotides may be of considerable length, e.g. if
using cDNA (which is encompassed within the scope of the
term "oligonucleotide"). The identification of such
10   cDNA molecules as useful probes allows the development
of shorter oligonucleotides which reflect the
specificity of the cDNA molecules but are easier to
manufacture and manipulate.

The above described model may then be used to
15   generate and analyse data of test samples and thus may
be used for the diagnostic methods of the invention. In
such methods the data generated from the test sample
provides the gene expression data set and this is
normalized and standardized as described above. This is
20   then fitted to the calibration model described above to
provide classification.

The method described herein can also be used to
simultaneously select informative probes for several
related and unrelated diseases or conditions. Depending
25   upon which diseases or conditions have been included in
the calibration or training set, informative probes can
be selected for the said diseases or conditions. The
informative probes selected for one disease or condition
may or may not be similar to the informative probes
30   selected for another disease or condition of interest.
It is the pattern with which the selected genes are
expressed in relation to each other during a disease,
condition, or stage thereof, that determines whether or
not they are informative for the disease, condition or
35   stage thereof.

In other words, informative genes are selected
based on how their expression correlates with the

- 54 -

expression of other selected informative genes under the
influence of responses generated by the disease,
condition or stage thereof under investigation. In
examples 1 and 2 provided hereinafter, 139 informative
5   probes were selected for breast cancer diagnosis and 182
probes were selected for Alzheimer's disease diagnosis
by training the gene expression data set of genes
representing 1435 or 758 randomly picked cDNA clones for
breast cancer/non breast cancer samples, or
10   Alzheimer/non-Alzheimer samples, respectively. Among
the probes selected for breast cancer and Alzheimer,
about 10 probes were informative both for breast cancer
and Alzheimer disease diagnosis.

     For the purpose of isolating informative probes or
15   identifying several related and unrelated diseases,
conditions and stages thereof simultaneously, the gene
expression data set must contain the information on how
genes are expressed when the subject has a particular
disease, condition or stage thereof under investigation.
20   The data set is generated from a set of healthy or
diseased samples, where a particular sample may contain
the information of only one disease, condition or stages
thereof or may also contain information about multiple
diseases, conditions or stages thereof. For example, if
25   the isolation of informative probes for Alzheimer
disease, breast cancer and diabetes is sought, whole
blood samples can be obtained from an Alzheimer patient
who has breast cancer and diabetes. Hence, the method
also teaches an efficient experimental design to reduce
30   the number of samples required for isolating informative
probes by selecting samples representing more than one
disease, condition or stage thereof.

     As mentioned previously, in view of the high
information content of most transcripts, the
35   identification and selection of informative probes for
use in diagnosing, monitoring or identifying a
particular disease, condition or stage thereof may be

- 55 -

dramatically simplified. Thus the pool of genes from
which a selection may be made to identify informative
probes may be radically reduced.

5   Unlike, in prior art technologies where informative
probes are selected from a population of thousands of
genes that are being expressed in a cell, like in
microarray, in the method described herein, the
informative probes are selected from a limited number of
randomly obtained genes. For example, from a population
10   of 1435 cDNA clones, randomly picked from a human whole
blood cDNA library, we were able to select 139
informative probes for breast cancer diagnosis (see
Example 1 and Table 2).

Thus in a preferred aspect of the above mentioned
15   method of identifying probes useful for diagnosing or
identifying or monitoring a disease or condition or
stage thereof in an organism, said set of
oligonucleotides which are immobilized in step (a) are
randomly selected from a larger set of oligonucleotides,
20   e.g. from a cDNA library or other oligonucleotide pool,
which may be, but is preferably not selected from the
set provided herein. Preferably said larger set
comprises oligonucleotides which correspond to
moderately or highly expressed genes. Thus preferably
25   in methods of the invention, the set of oligonucleotides
according to the invention are replaced with a set of
oligonucleotides which are randomly selected, e.g. from
commercially available oligonucleotide or cDNA
libraries.

30   As referred to herein "random" refers to selection
which is not biased based on the extent of information
carried by the transcripts in relation to the disease,
condition or organism under study, ie. without bias
towards their likely utility as informative probes.
35   Whilst a random selection may be made from a pool of
transcripts (or related products) which have been
biased, e.g. to highly or moderately expressed

transcripts, preferably random selection is made from a pool of transcripts not biased or selected by a sequence-based criterion. The larger set may therefore contain oligonucleotides corresponding to highly and moderately expressed genes, or alternatively, may be enriched for those corresponding to the highly and moderately expressed genes.

Random selection from highly and moderately expressed genes can be achieved in a wide variety of ways. A strategy used in this work, but not limiting in itself involves randomly picking a significant number of cDNA clones from a cDNA library constructed from a biological specimen under investigation. Since, in a cDNA library, the cDNA clones corresponding to transcripts present in high or moderate amount are more frequently present than transcripts corresponding to cDNA present in low amount, the former will tend to be picked up more frequently than the latter. A pool of cDNA enriched for those corresponding to highly and moderately expressed genes can be isolated by this approach.

To identify genes that are expressed in high or moderate amount among the isolated population for use in methods of the invention, the information about the relative level of their transcripts in samples of interest can be generated using several prior art techniques. Both non-sequence based methods, such as differential display or RNA fingerprinting, and sequence-based methods such as microarrays or macroarrays can be used for the purpose. Alternatively, specific primer sequences for highly and moderately expressed genes can be designed and methods such as quantitative RT-PCR can be used to determine the levels of highly and moderately expressed genes. Hence, a skilled practitioner may use a variety of techniques which are known in the art for determining the relative level of mRNA in a biological sample.

- 57 -

Especially preferably the sample for the isolation
of mRNA in the above described method is as described
previously and is preferably not from the site of
disease and the cells in said sample are not disease
5   cells and have not contacted disease cells.

The following examples are given by way of
illustration only in which the Figures referred to are
as follows:

Figure 1 shows the effect of Direct Standardization
10   (DS) on the Alzheimer data measured in two different
series of experiments in which AD denotes Alzheimer's
samples and A,B are non-Alzheimer's samples. The
samples in both series have been labelled systematically
as (xx_7/xx_8), whereas the corrected samples from
15   series 8 (in b,c,d) have been labelled as (xx_c), thus,
for example, AD2-7 denotes Alzheimer disease sample
number 2 in experiment series 7. The circled spots
represent the samples chosen as the transfer samples.
The connecting lines in figures b,c,d show the proximity
20   of the replicated samples after applying DS. The dashed
lines in figures a,c,d represent the decision boundary
separating the classes. These lines have not been drawn
on the basis of any statistical criteria, but serve the
purpose of visually separating the classes. All the
25   four figures show scores plot (PC1-PC2) from PCA
analysis based on (a) non-standardized data, (b) scores
plot after direct standardization using 3 transfer
samples, (c) scores plot after direct standardization
using 4 transfer sample, (d) scores plot after direct
30   standardization using 8 transfer samples;

Figure 2 shows the projection of normal (including
benign) and breast cancer samples onto a classification
model generated by PLSR-DA using the data of 44
informative genes, in which PC is the principal
35   components and N and C are normal and breast cancer
samples, respectively;

Figure 3 shows the projection of individuals with

- 58 -

and without Alzheimer's disease onto a classification
model generated by PLSR-DA using 182 informative genes;

Figures 4, 6 and 8 show projection plots as Figure
2 in which the classification model is generated using
5   719, 111 and 345 cDNAs, respectively, wherein PC is the
principal components, N denotes normal and B denotes
breast cancer samples;

Figures 5, 7 and 9 show prediction plots based on 3
principal components using the data of 719, 111 and 345
10   cDNAs, respectively;

Figure 10 shows a projection plot as Figure 3 in
which the classification model is generated using 520
cDNAs; and

Figure 11 is the prediction plot corresponding to
15   Figure 10.

Example 1: Diagnosis of Breast Cancer

Methods

20

Whole blood was obtained from the arms of breast cancer
patients and patients with benign tumours (Ullevål and
Haukland hospitals in Norway). All of the patients with
breast cancer had a malignant tumour of the breast
25   (disease samples). Healthy blood was collected from the
above two hospitals, or collected at a Health station at
Ås, Norway or at DiaGenic AS, Norway, from the arms of
female donors with no reported signs of breast cancer.
The blood from healthy individuals or with benign
30   tumours comprise the normal samples. The blood was
either collected in tubes containing EDTA and stored
immediately at -80°C or was collected in PAXgene tubes
and stored for 12-24 hours at room temperature before
finally storing them at -80°C before use. Further
35   details of the breast cancer and benign tumour patients
from which blood was taken is provided in Table 5.

mRNA was isolated from the blood of the 29 breast cancer
patients and 46 normal donors and used to prepare
labelled probes by reverse transcribing in the presence
of $\alpha^{33}P$-dATP. The first strand cDNA of the normal and

5   diseased samples was bound, separately to 1435 cDNA
clones immobilized on a solid support (nylon membrane).
These cDNA clones were randomly picked, without any
prior knowledge of their gene sequences, from a cDNA
library constructed using whole blood of 550 healthy

10   individuals (Clontech, Palo Alto, USA). These methods
were conducted as follows.

For amplification of inserts, bacterial clones were
grown in microtiter plates containing 150 μl LB with 50

15   μg/ml carbenicillin, and incubated overnight with
agitation at 37°C. To lyse the cells, 5 μl of each
culture were diluted with 50 μl H2O and incubated for 12
min. at 95°C. Of this mixture, 2 μl were subjected to a
PCR reaction using 20 pmoles of M13 forward and reverse

20   primer in presence of 1.5 mM $MgCl_2$. PCR reactions were
performed with the following cycling protocol: 4 min. at
95°C, followed by 25 cycles of 1 min. at 94°C, 1 min. at
60°C and 3 min. at 72°C either in a RoboCycler®
Temperature Cycler (Stratagene, La Jolla, USA) or DNA

25   Engine Dyad Peltier Thermal Cycler (MJ Research Inc.,
Waltham, USA). The amplified products were denatured by
incubating with NaOH (0.2 M, final concentration) for 30
min. and spotted onto Hybond-N+ membranes (Amersham
Pharmacia Biotech, Little Chalfont, UK), using MicroGrid

30   II workstation according to the manufacturer's
instructions (BioRobotics Ltd, Cambridge England). The
immobilized cDNAs were fixed using a UV cross-linker
(Hoefer Scientific Instruments, San Francisco, USA).

35   In addition to the 1435 cDNAs, the printed arrays also
contained controls for assessing background level,
consistency and sensitivity of the assay. These were

- 60 -

spotted at multiple positions and included controls such
as PCR mix (without any insert); positive and negative
controls of SpotReportTM 10 array validation system
(Stratagene, La Jolla, USA) and cDNAs corresponding to
5   constitutively expressed genes such as b-actin, g-actin,
GAPDH, HOD and cyclophilin. Also, oligonucleotides
corresponding to SIX1, b-tubulin, TRP-2, MDM2, Myosin
Light C, CD44, Maspin, Laminin, and SRP 19 were included
to detect disseminated cancer cells.
10

The total RNA from blood collected in EDTA tubes was
purified using Trizol LS Reagent protocol
(Invitrogen/Life Technologies). From blood contained in
PAXgene tubes, the total RNA was purified according to
15   the supplier's instructions (PreAnalytiX, Hombrechtikon,
Switzerland). Contaminating DNA was removed from the
isolated RNA by DNAase I treatment using DNA-free kit
(Ambion, Inc. Austin, USA). RNA quality was determined
visually by inspecting the integrity of 28S and 18S
20   ribosomal bands following agarose gel electrophoresis.
The concentration and purity of extracted RNA was
determined by measuring the absorbance at 260 nm and 280
nm. mRNA was isolated from the total RNA using Dynabeads
as per the supplier's instructions (Dynal AS, Oslo,
25   Norway).

Labelling and hybridization experiments were performed
in batches. The number of samples assayed in each batch
varied from six to nine. In the case of samples that
30   were assayed more than once (replicates), aliquots
derived from the same mRNA pool were used for probe
synthesis. For probe synthesis, aliquots of mRNA
corresponding to 4-5 μg of total RNA were mixed together
with oligodT$_{25NV}$ (0.5 μg/ml) and mRNA spikes of
35   SpotReport™ 10 array validation system (10 pg; Spike 2,
1 pg), heated to 70°C to remove secondary structures,
and then chilled on ice. Probes were prepared in 35μl

reaction mixes by reverse transcription in the presence
of 50μCi [α^{33}P] dATP, 3.5 μM dATP, 0.6 mM each of dCTP,
dTTP, dGTP, 200 units of SuperScript reverse
transcriptase (Invitrogen, LifeTechnologies) and 0.1 M
5   DTT, labelling for 1.5 hr at 42°C. Following synthesis,
the enzyme was deactivated for 10 min. at 70°C and mRNA
removed by incubating the reaction mix for 20 min. at
37°C in 4 units of Ribo H (Promega, Madison USA).
Unincorporated nucleotides were removed using ProbeQuant
10   G 50 Columns (Amersham Biosciences, Piscataway, USA).

Prior to hybridization, the membranes were equilibrated
in 4 x SSC for 2 hr at room temperature and
prehybridized overnight at 65°C in 10 ml
15   prehybridisation solution (4 x SSC, 0.1 M NaH$_2$PO$_4$, 1 mM
EDTA, 8% dextran sulphate, 10 x denhardt's solution, 1%
SDS). Freshly prepared probes were added to 5 ml of the
same prehybridisation solution, and hybridization
continued overnight at 65°C. The membranes were washed
20   at 65°C at increasing stringency (2 x 30 min. each in 2
x SSC, 0.1% SDS; 1 x SSC, 0.1% SDS; 0.1 x SSC, 0.1% SDS)
to remove unspecific signals.

The amount of labelled first strand cDNA binding to each
25   spot was assessed and quantified using a PhosphoImager
to generate a gene expression data set. The data was
generated using Phoretix software version 3 (Non Linear
Dynamics, England). Background subtraction was
performed on the generated data by subtracting the
30   median of the line of pixels around each spot outline
from the total intensity obtained from the respective
spots.

The background-subtracted data was then normalized and
35   transformed by selecting out 50 lowest and 50 maximum
signals from each membrane. This step was to exclude
genes that were expressed with a high degree of

variance.   Since the genes varied from membrane to
membrane, the expression data from 497 genes were
removed from the data set.   The values for the remaining
938 genes were then normalised by using different
5   approaches such as external controls, dividing each spot
by the median intensity of the observed signal in the
respective membrane, range normalizing the data from
each membrane, and then log transforming the data
obtained.
10

The processed data obtained above was then used to
isolate the informative probes by:
     a) keeping one unique sample (including all
repetitions of the selected sample) out per cross
15   validation segment;
     b) building a calibration model (cross validated)
on the remaining samples using PLSR-DA;
     c) selecting the set of significant genes for the
model in step b using the Jackknife criterion;
20   d) repeating steps a), b) and c) until all the
unique samples were kept out once (hence, in all 75
different calibration models were built (after repeating
step b) 75 times), resulting in 75 different sets of
significant probes (after repeating step c) 75 times));
25   e)   selecting significant variables using the
frequency of occurrence criterion amongst the 75
different sets of significant probes.

     The selected informative probes based on occurrence
30   criterion were used to construct a classification model.
The result of the classification model based on probes
appearing in at least 90% of the generated sets after
the step of isolating informative probes as described
above is shown in Figure 2 in which it is seen that the
35   expression pattern of these genes was able to classify
most women with breast cancer and women with no breast
cancer into distinct groups.   In this figure PC1 and PC2

indicate the two principal components statistically derived from the data which best define the systemic variability present in the data. This allows each sample, and the data from each of the informative probes

5   to which the sample's labelled first strand cDNA was bound, to be represented on the classification model as a single point which is a projection of the sample onto the principal components - the score plot.

10   The ability of the generated model, based on isolated informative probes, to predict future samples was determined by the double cross-validation approach. The performance of the diagnostic test for breast cancer based on the occurrence criterion is presented in Table

15   6.

Correct prediction of most breast cancer cells was achieved. These included all three samples obtained from women with ductal carcinoma in situ (DCIS), 11/15

20   samples obtained from women with stage I breast cancer, all five samples obtained from women with stage II breast cancer, and one of two samples obtained from women with stage III breast cancer. Interestingly, two correctly predicted stage I samples were obtained from

25   women having a tumour size of <5 mm in diameter.

The model also correctly predicted the class of most non-cancer samples (41/46), including those that were obtained from women with non-cancerous breast

30   abnormalities.

Confirmation that the gene transcripts are not from cells which are disseminated disease cells has been confirmed by several lines of evidences. Firstly, the

35   informative genes were expressed constitutively at high or moderate levels in blood cells of women irrespective of whether they had cancer or not. Secondly, in the

assay described in this Example, in order to identify
transcripts, at least 720 disseminated cells in blood
samples would be required. Since, the average number of
disseminated cells present in blood during different

5   stages of breast cancer is much lower (organ confined
breast cancer, 0.8 cells per ml; invasive breast cancer
spread to lymph nodes only, 2.4 cells per ml; and
metastatic breast cancer, 6 cells per ml; SD>100%) (29),
we believe that the signals being detected originated

10   from peripheral blood cells and could not have
originated from disseminated cells. Thirdly, we were
not able to detect any signal from the eight cancer
markers known to have elevated expression in malignant
cancer cells, including cancer cells that are

15   disseminated in the blood.

Example 2: Diagnosis of Alzheimer's disease

Similar experiments were conducted with samples from
20   Alzheimer's patients. In this method 7 patients
diagnosed with Alzheimer's Disease at the Memory Clinic
at Ulleval University Hospital were used in the trial.
The patients were confirmed as having Alzheimer's
disease based on the following criteria:

25   *   A standardized interview with a care-giver using
          IQCODE, an ADL scale and a scale measuring
          behaviour of the patient (Green scale).
     *   Neuropsychological evaluation using MMSE, Clock
          drawing test, Trailmaking test A and B (TMT A and
30   B), Kendrick object learning test (visual memory
          test), part of the Wechsler battery and Benton
          test.
     *   A psychiatric evaluation using scales for detection
          of depression, MADRS for interviewing the patient
35   and Cornell scale for interviewing the care-giver.
     *   A physical examination.
     *   Laboratory tests of blood samples to rule out other

- 65 -

        diseases.
*   CT scan of the brain.
*   SPECT of the brain.

5   The mean age of the patients was 72.3 with an age range
    of 69-76. The mean MMSE score was 22.0 (the maximum
    score attainable being 30).

    Six age-matched individuals without diagnosed
10 Alzheimer's disease were used as a control. All had
    been tested with MMSE and had a minimum score of 28
    (mean: 28.4). The mean age of the normal control group
    was 73.0 and the age range 66-81. A sample from a 16-
    year old individual, with a consequent minimal chance of
15 having Alzheimer's disease, was also included as an
    additional control.

    Using the methods described above (except that
    hybridization to 758 rather than 1435 cDNA clones was
20 performed), informative probes were selected based on
    occurrence criterion and used to construct a
    classification model. The results of the classification
    model based on probes appearing at least once in the
    generated sets after the method to isolate informative
25 probes as described above is shown in Figure 3 in which
    it will be seen that the expression pattern of these
    genes was able to classify individuals with or without
    Alzheimer's disease into distinct groups. In this
    Figure PC1 and PC2 indicate the 2 principal components
30 statistically derived from the data which define the
    systematic variability present in the data. This allows
    each sample, and the data from each of the informative
    probes to which the samples' cDNA was bound, to be
    represented on the classification model as a single
35 point which is a projection of the sample onto the
    principal components - the score plot.

- 66 -

The ability of the generated model, based on isolated
informative probes, to predict future samples was
determined by the double cross-validation. The
performance of the diagnostic test for Alzheimer's
disease is presented in Table 7.

- 67 -

Appendix A

Partial Least Squares regression (PLSR)

5   Let a multivariate regression model be defined as:

$$Y = XB + F$$

where
10   X a NxP matrix with N predictor variables (genes);
Y (NxJ) being the J predicted variables. In our case Y
represents a matrix containing dummy variables;
B is a matrix of regression coefficients; and
F is a NxJ matrix of residuals.
15

The structure of the PLSR model can be written as:

$$X = TP^T + E_A, \text{ and}$$
$$Y = TQ^T + F_A, \text{ where}$$
20

where
T (NxA) is a matrix of score vectors which are linear
combinations of the x-variables;
P (PxA) is a matrix with the x-loading vectors p_a as
25   columns;
Q (JxA) is a matrix with the y-loading vectors q_a as
columns;
E_a (NxP) is the matrix for X after A factors; and
F_a (NxJ) is the matrix for Y after A factors.
30

The criterion in PLSR is to maximize the explained
covariance of [X,Y]. This is achieved by the loading
weights vector w_{a+1}, which is the first eigenvector of
$E_a^T F_a F_a^T E_a$ (E_a and F_a are the deflated X and Y after a
35   factors or PLS components).

The regression coefficients are given by:

$$B = W(P^TW)^{-1}Q^T$$

A PLSR model with full rank, i.e. maximum number of components, is equivalent to the MLR solutions. Further details on PLSR can be found in Marteus & Naes, 1989, Multivariate Calibration, John Wiley & Sons, Inc., USA and Kowalski & Seasholtz, 1991, supra.

- 69 -

Example 3: Validation of Example 1, diagnosis of breast cancer

The results in Example 1 were validated by using the informative probes identified in Example 1 on new beast cancer and control samples.

Methods
The methods, essentially as described in Example 1, were used. Blood was taken from patients as described in Table 8. However, blood was collected in PAXgene tubes and the first strand labelled cDNAs were hybridized to 719 cDNAs spotted on nylon membranes along with other controls as described in Example 1. After background subtraction using control spots, the data of each membrane was normalized using the inter quantile range. The data was analysed as described in Example 1 and the model validated by cross validation.

The 719 cDNAs which were spotted are a subset of the cDNAs spotted in Example 1 and include 111 cDNAs described in Table 2 and which were found to be informative in Example 1.

Results
The results are shown in Figures 4 to 9. Figures 4, 6 and 8 are projection plots similar to Figure 2 and show the projection of normal and breast cancer patients' samples onto a classification model generated using all 719 cDNA. Figure 6 is similar but uses a classification model generated with the 111 probes common to Example 1. Figure 8 uses the 345 sequences of the 719 for which sequence information is provided herein. In each case classification of normal and breast cancer groups was possible. Figures 5, 7 and 9 show prediction plots which reflect the ability of the generated models to correctly diagnose breast cancer. In the 3 prediction

- 70 -

plots shown, the disease samples appear on the x axis at
+1 and the non-disease samples appear at -1. The y axis
represents the predicted class membership. During
prediction, if the prediction is correct, disease
5   samples should fall above zero and non-disease samples
should fall below zero. In each case almost all samples
are correctly predicted.

Example 4: Validation of Example 2, diagnosis of
10   Alzheimers

The results in Example 2 were validated by using the
informative probes identified in Example 2 on new
Alzheimer's patient samples.

15

Methods
The methods, essentially as described in Example 2, were
used. Twelve female patients diagnosed with Alzheimer's
disease at the Memory Clinic at Ulleval University
20   Hospital who were confirmed as having Alzheimer's
disease based on the criteria of Example 2 were used in
the trial. The mean age of the patients was 72.3 with
an age range of 66-83. The mean MMSE score was 22.0
(the maximum score attainable being 30).

25

Sixteen age-matched female individuals without diagnosed
Alzheimer's disease were used as the normal control
group. All had been tested with MMSE and had a minimum
score of 29. The mean age of the normal control group
30   was 74.0 and the age range 66-86.

After transfer of the blood to PAXgene tubes, total mRNA
was isolated from the blood of the Alzheimer's disease
and from the control group donors according to the
35   manufacturers's instructions (PreAnalytiX,
Hombrechtikon, Switzerland). The isolated mRNA was
labelled during reverse transcription in the presence of

- 71 -

α^{33}P-dATP, yielding a labelled first strand cDNA. Hybridization was performed as described previously onto 730 cDNA clones picked from a cDNA library from whole blood of 550 healthy individuals without knowledge of
5   the gene sequence of the random cDNA clones.

<u>Results</u>

The results are shown in Figures 10 and 11. Figure 10 is a projection plot generated using 520 probes which
10   have been sequenced. Figure 11 is a prediction plot and shows correct prediction of almost all samples.

72

Table 1a

List of probes informative for disease diagnosis

	Clone ID	Sequence ID	No. of nucleotides
1	I-01	-	-
2	I-02	-	-
3	I-13	-	-
4	I-21	-	-
5	I-24	308	373
6	I-28	310	564
7	I-30	1180	622
8	I-34	313	554
9	I-37	-	-
10	I-42	-	-
11	I-52	-	-
12	I-54	1181	155
13	I-58	326	554
14	I-71	-	-
15	I-72	-	-
16	I-86	-	-
17	I-95	-	-
18	II-03	361	622
19	II-05	363	628
20	II-06	364	528
21	II-10	368	329
22	II-24	381	534
23	II-25	382	444
24	II-26	383	566
25	II-33	390	523
26	II-34	391	566
27	II-41	397	534
28	II-42	398	512
29	II-47	-	-
30	II-57	411	505
31	II-61	415	596
32	II-69	423	387
33	II-70	424	420
34	II-75	429	535
35	II-83	-	-
36	II-84	438	577
37	II-87	441	552
38	II-88	442	606
39	II-90	-	-
40	II-94	448	329
41	III-02	453	747
42	III-05	-	-
43	III-06	458	682

44	III-08	460	536
45	III-10	-	-
46	III-13	464	615
47	III-15	-	-
48	III-17	-	-
49	III-20	1183	479
50	III-23	473	694
51	III-26	476	476
52	III-35	485	551
53	III-39	487	224
54	III-40	488	349
55	III-43	490	382
56	III-44	491	382
57	III-53	500	390
58	III-56	503	109
59	III-57	504	374
60	III-60	-	-
61	III-60	-	-
62	III-61	507	521
63	III-63	509	575
64	III-68	-	-
65	III-74	518	502
66	III-80	523	585
67	III-82	-	-
68	III-85	526	516
69	III-89	530	660
70	III-92	-	-
71	III-96	-	-
72	IV-14	684	545
73	IV-15	1185	628
74	IV-23	-	-
76	IV-26	1186	494
75	IV-26	-	-
77	IV-29	-	-
78	IV-31	687	268
79	IV-32	688	569
80	IV-34	-	-
81	IV-35	-	-
82	IV-41	-	-
83	IV-45	-	-
84	IV-53	61	362
85	IV-62	-	-
86	IV-69	192	286
87	IV-80	701	579
88	IV-82	-	-
89	IV-93	-	-
90	IX-10	736	641
91	IX-12	-	-
92	IX-38	757	583
93	IX-39	758	424
94	IX-42	-	-
95	IX-48	764	626
96	IX-77	785	556
97	V-01	-	-
98	V-02	-	-
99	V-03	706	496

100	V-04	707	397
101	V-06	-	-
102	V-07	708	293
103	V-11	1188	599
104	V-12	711	498
105	V-15	-	-
106	V-17	-	-
107	V-21	-	-
108	V-25	-	-
109	V-32	-	-
110	V-35	-	-
111	V-39	-	-
112	V-42	-	-
113	V-43	-	-
114	V-47	-	-
115	V-49	-	-
116	V-52	-	-
117	V-54	-	-
118	V-55	77	412
119	V-58	-	-
120	V-59	-	-
121	V-65	-	-
122	V-68	-	-
123	V-71	-	-
124	V-75	-	-
125	V-79	-	-
126	V-80	726	260
127	V-90	-	-
128	V-91	-	-
129	V-92	-	-
130	V-94	-	-
131	VI-02	-	-
132	VI-04	865	122
133	VI-07	93	405
134	VI-09	-	-
135	VI-10	-	-
136	VI-12	869	667
137	VI-14	871	642
138	VI-17	-	-
139	VI-20	876	115
140	VI-21	-	-
141	VI-23	878	634
142	VI-34	-	-
143	VI-41	-	-
144	VI-42	-	-
145	VI-43	-	-
146	VI-44	-	-
147	VI-48	891	626
148	VI-49	-	-
149	VI-50	893	585
150	VI-52	-	-
151	VI-53	895	560
152	VI-55	897	509
153	VI-65	-	-
154	VI-70	108	550
155	VI-71	-	-

156	VI-72	-	-
157	VI-74	905	655
158	VI-76	907	582
159	VI-78	-	-
160	VI-79	-	-
161	VI-84	-	-
162	VI-87	911	595
163	VI-88	912	651
164	VI-90	-	-
165	VI-93	-	-
166	VI-95	915	230
167	VI-96	-	-
168	VII-02	-	-
169	VII-03	1196	412
170	VII-06	-	-
171	VII-10	-	-
172	VII-11	-	-
173	VII-15	1199	439
174	VII-19	562	580
175	VII-21	564	671
176	VII-25	-	-
177	VII-32	571	457
178	VII-36	575	209
179	VII-39	576	541
180	VII-42	579	502
181	VII-43	580	316
182	VII-46	583	631
183	VII-47	1200	526
184	VII-48	1201	613
185	VII-59	593	565
186	VII-60	-	-
187	VII-63	595	98
188	VII-66	598	362
189	VII-67	-	-
190	VII-72	600	595
191	VII-73	601	522
192	VII-75	-	-
193	VII-76	603	624
194	VII-77	1203	692
195	VII-80	605	338
196	VII-81	606	556
197	VII-83	-	-
198	VII-86	-	-
199	VII-88	-	-
200	VII-90	612	576
201	VII-91	613	341
202	VII-93	615	379
203	VIII-01	-	-
204	VIII-02	-	-
205	VIII-03	-	-
206	VIII-06	-	-
207	VIII-09	618	598
208	VIII-10	-	-
209	VIII-15	-	-
210	VIII-20	628	419
211	VIII-22	-	-

212	VIII-26	-	-
213	VIII-28	634	511
214	VIII-29	635	592
215	VIII-30	636	572
216	VIII-31	637	482
217	VIII-32	638	545
218	VIII-33	639	624
219	VIII-39	-	-
220	VIII-41	645	649
221	VIII-42	646	600
222	VIII-44	-	-
223	VIII-46	649	425
224	VIII-48	651	251
225	VIII-58	-	-
226	VIII-64	663	627
227	VIII-65	-	-
228	VIII-66	665	345
229	VIII-67	666	252
230	VIII-74	-	-
231	VIII-76	675	591
232	VIII-78	-	-
233	VIII-82	-	-
234	VIII-83	-	-
235	VIII-85	-	-
236	VIII-87	-	-
237	VIII-91	-	-
238	VIII-92	-	-
239	VIII-93	-	-
240	VIII-95	-	-
241	X-04	-	-
242	X-07	808	641
243	X-15	814	132
244	X-29	821	370
245	X-34	-	-
246	X-35	-	-
247	X-54	837	603
248	X-56	839	71
249	X-68	1207	642
250	X-72	849	622
251	X-94	860	501
252	XI-07	-	-
253	XI-13	1209	620
254	XI-50	-	-
255	XI-58	-	-
256	XI-81	1212	374
257	XII-07	1213	567
258	XII-17	-	-
259	XII-26	-	-
260	XII-27	-	-
261	XII-31	-	-
262	XII-32	-	-
263	XII-35	1214	620
264	XII-36	-	-
265	XII-52	-	-
266	XII-59	1216	484
267	XIII-19	1219	559

268	XIII-29	-	-
269	XIII-52	939	513
270	XIII-62	-	-
271	XIII-84	-	-
272	XIII-92	1221	741
273	XV-18	-	-
274	XV-22	1099	561
275	XV-24	-	-
276	XV-25	1224	485
277	XV-28	-	-
278	XV-34	-	-
279	XV-42	-	-
280	XV-68	-	-
281	XV-74	-	-
282	XV-93	-	-
283	XV-94	-	-
284	XV-96	-	-
285	XVI-36	1056	435
286	XVI-53	1230	741
287	XVI-59	-	-
288	XVI-66	1074	689
289	XVI-76	1083	198
290	XVI-77	1084	198
291	XVII-07	-	-
292	XVII-08	-	-
293	XVII-17	-	-
294	XVII-28	-	-
295	XVII-29	-	-
296	XVII-31	1139	503
297	XVII-36	-	-
298	XVII-39	-	-
299	XVII-40	1231	203
300	XVII-48	1148	587
301	XVII-55	-	-
302	XVII-58	-	-
303	XVII-67	-	-
304	XVII-72	-	-
305	XVII-76	1160	650
306	XVII-82	-	-
307	XVII-87	1165	502
308	XVII-95	1172	648

Table 1 b

List of sequences of probes informative for disease diagnosis

Please see the note at the bottom

Clone ID	Sequence ID
I-09	298
I-10	299
I-13	1331
I-14	1178
I-15	300
I-16	301
I-17	302
I-19	304
I-20	305
I-22	306
I-23	307
I-24	308
I-25	309
I-28	310
I-30	1180
I-31	311
I-32	312
I-34	313
I-37	1440
I-38	314
I-39	315
I-40	316
I-42	1332
I-44	317
I-45	318
I-46	319
I-47	320
I-48	321
I-49	322
I-53	323
I-54	1181
I-56	324
I-57	325
I-58	326
I-60	327
I-64	328
I-67	330
I-69	331
I-71	332
I-72	333
I-73	334
I-77	335
I-79	336
I-80	337

I-81		338
I-82		339
I-86		1336
I-88		1182
I-95		1337
II-02		360
II-03		361
II-05		363
II-06		364
II-07		365
II-08		366
II-09		367
II-10		368
II-11		369
II-12		370
II-13		371
II-14		372
II-15		373
II-16		374
II-17		375
II-18		376
II-20		377
II-21		378
II-22		379
II-23		380
II-24		381
II-25		382
II-26		383
II-27		384
II-28		385
II-29		386
II-30		387
II-31		388
II-32		389
II-33		390
II-34		391
II-35		392
II-37		393
II-38		394
II-39		395
II-40		396
II-41		397
II-42		398
II-43		399
II-44		400
II-46		401
II-47		402
II-48		403
II-49		404
II-50		405
II-52		406

II-53	407
II-54	408
II-55	409
II-56	410
II-57	411
II-58	412
II-59	413
II-60	414
II-61	415
II-62	416
II-63	417
II-64	418
II-65	419
II-66	420
II-67	421
II-68	422
II-69	423
II-70	424
II-71	425
II-72	426
II-73	427
II-74	428
II-75	429
II-76	430
II-77	431
II-78	432
II-79	433
II-80	434
II-81	435
II-82	436
II-83	437
II-84	438
II-85	439
II-86	440
II-87	441
II-88	442
II-89	443
II-90	444
II-91	445
II-92	446
II-93	447
II-94	448
II-95	449
II-96	450
III-01	452
III-02	453
III-03	454
III-04	455
III-05	457
III-06	458
III-07	459

III-08	460
III-09	461
III-11	462
III-12	463
III-13	464
III-14	465
III-15	466
III-16	467
III-17	468
III-18	469
III-19	470
III-20	1183
III-21	471
III-22	472
III-23	473
III-24	474
III-25	475
III-26	476
III-27	477
III-28	478
III-29	479
III-31	481
III-32	482
III-33	483
III-34	484
III-35	485
III-37	486
III-39	487
III-40	488
III-42	489
III-43	490
III-44	491
III-45	492
III-46	493
III-47	494
III-48	495
III-49	496
III-50	497
III-51	498
III-52	499
III-53	500
III-54	501
III-55	502
III-56	503
III-57	504
III-58	505
III-59	506
III-61	507
III-62	508
III-63	509
III-64	510

III-65		511
III-66		512
III-67		513
III-69		514
III-70		515
III-71		516
III-73		517
III-74		518
III-75		519
III-77		520
III-78		521
III-79		522
III-80		523
III-81		524
III-82		1348
III-83		525
III-85		526
III-86		527
III-87		528
III-88		529
III-89		530
III-91		531
III-92		1351
III-93		532
III-94		533
III-95		534
III-96		535
IV-02		681
IV-04		682
IV-13		683
IV-14		684
IV-15		1185
IV-17		685
IV-23		1353
IV-26		1186
IV-28		686
IV-31		687
IV-32		688
IV-35		1355
IV-37	g6	
IV-38		689
IV-40		690
IV-42		691
IV-43		1239
IV-44		692
IV-47		693
IV-53		61
IV-55		694
IV-56		695
IV-61		696
IV-64		697

IV-65	698
IV-69	192
IV-72	699
IV-73	700
IV-80	701
IV-82	196
IV-85	702
IV-93	703
IV-95	704
IV-96	705
IX-10	736
IX-12	738
IX-13	739
IX-24	747
IX-38	757
IX-39	758
IX-48	764
IX-50	766
IX-56	768
IX-62	773
IX-65	776
IX-72	782
IX-77	785
IX-91	796
IX-96	801
V-01	1361
V-03	706
V-04	707
V-07	708
V-08	709
V-09	710
V-11	1188
V1-16	873
V1-19	875
V-12	711
V-17	1364
V-18	712
V-20	713
V-24	714
V-25	1365
V-28	1189
V-35	1366
V-37	716
V-38	1190
V-39	1109
V-40	717
V-41	718
V-47	1368
V-48	719
V-49	1369
V-55	77

V-57	720
V-58	1370
V-61	721
V-64	722
V-65	723
V-68	1448
V-71	1495
V-74	724
V-75	1372
V-80	726
V-81	727
V-87	728
V-90	1374
VI-02	340
VI-03	341
VI-04	342
VI-06	343
VI-07	344
VI-08	345
VI-09	346
VI-11	347
VI-12	869
VI-13	870
VI-14	871
VI-16	873
VI-18	348
VI-19	349
VI-20	350
VI-21	351
VI-22	352
VI-23	878
VI-24	879
VI-25	353
VI-26	354
VI-27	355
VI-31	356
VI-32	885
VI-33	357
VI-35	358
VI-39	887
VI-43	1382
VI-44	1193
VI-45	889
VI-48	359
VI-49	892
VI-50	893
VI-53	895
VI-55	897
VI-58	899
VI-66	903
VI-67	904

VI-70	108
VI-71	1387
VI-74	905
VI-75	906
VI-76	907
VI-77	110
VI-79	1389
VI-80	908
VI-85	910
VI-87	911
VI-88	912
VI-90	1390
VI-93	1391
VI-95	915
VI-96	1392
VII-02	547
VII-03	548
VII-04	549
VII-05	550
VII-06	551
VII-07	552
VII-08	553
VII-09	554
VII-10	555
VII-11	556
VII-12	557
VII-14	558
VII-15	559
VII-17	560
VII-18	561
VII-19	562
VII-20	563
VII-21	564
VII-22	565
VII-23	566
VII-24	567
VII-25	1397
VII-26	250
VII-27	568
VII-28	569
VII-29	570
VII-32	571
VII-33	572
VII-34	573
VII-35	574
VII-36	575
VII-39	576
VII-40	577
VII-41	578
VII-42	579
VII-43	580

VII-44	581
VII-45	582
VII-46	583
VII-47	1200
VII-48	584
VII-49	585
VII-50	586
VII-52	587
VII-53	588
VII-54	589
VII-55	590
VII-57	591
VII-58	592
VII-59	593
VII-62	594
VII-63	595
VII-64	596
VII-65	597
VII-66	598
VII-67	1399
VII-71	599
VII-72	600
VII-73	601
VII-74	602
VII-76	603
VII-77	604
VII-80	605
VII-81	606
VII-82	607
VII-83	608
VII-84	609
VII-86	1453
VII-87	610
VII-89	611
VII-90	612
VII-91	613
VII-92	614
VII-93	615
VII-94	616
VII-96	617
VIII-09	618
VIII-10	619
VIII-11	620
VIII-12	621
VIII-13	622
VIII-15	623
VIII-16	624
VIII-17	625
VIII-18	626
VIII-19	627
VIII-20	628

VIII-21	629
VIII-22	1455
VIII-23	630
VIII-24	631
VIII-25	632
VIII-26	1456
VIII-27	633
VIII-28	634
VIII-29	635
VIII-30	636
VIII-31	637
VIII-32	638
VIII-33	639
VIII-34	640
VIII-36	641
VIII-37	642
VIII-38	643
VIII-40	644
VIII-41	645
VIII-42	646
VIII-43	647
VIII-45	648
VIII-46	649
VIII-47	650
VIII-48	651
VIII-50	652
VIII-51	653
VIII-53	654
VIII-54	655
VIII-55	656
VIII-56	657
VIII-57	658
VIII-58	659
VIII-59	660
VIII-60	661
VIII-61	662
VIII-64	663
VIII-65	664
VIII-66	665
VIII-67	666
VIII-68	667
VIII-69	668
VIII-70	669
VIII-71	670
VIII-72	671
VIII-73	672
VIII-74	673
VIII-75	674
VIII-76	675
VIII-77	676
VIII-78	677

VIII-79	678
VIII-80	679
X-07	808
X-15	814
X-20	817
X-29	821
X-34	825
X-46	833
X-54	837
X-56	839
X-68	1207
X-72	849
X-73	1208
X-94	860
XI-13	1209
XI-37	1460
XI-43	1210
XI-67	1211
XI-81	1212
XII-07	1213
XII-35	1214
XII-36	1215
XII-59	1216
XII-65	1028
XII-92	1217
XIII-03	917
XIII-04	1218
XIII-19	1219
XIII-24	926
XIII-51	938
XIII-52	939
XIII-67	947
XIII-69	949
XIII-88	1220
XIII-92	1221
XV-22	1099
XV-24	1101
XV-25	1224
XV-42	1108
XV-62	1226
XV-64	1118
XV-84	1125
XVI-19	1228
XVI-36	1056
XVI-53	1230
XVI-60	1071
XVI-66	1074
XVI-74	1081
XVI-76	1083
XVI-77	1084
XVII-31	1139

XVII-40	1231
XVII-48	1148
XVII-76	1160
XVII-87	1165
XVII-95	1172

Note

Sequences not available for sequence IDs in Table 1, and corresponding sequence Ids in Table 2 and 4.

298,301,305,307,312,317,318,319,320,332,333,334,336,340,341,342,343,344,345,346,347,34
8,349,350,351,352,353,354,355,356,357,358,359,367,372,375,376,377,379,385,392,393,404,
437,439,440,443,444,445,449,455,457,465,466,467,468,470,486,498,501,511,514,516,517,52
0,522,528,531,535,547,548,549,550,551,552,553,554,555,556,557,558,559,573,584,604,608,
616,620,623,640,659,662,664,667,668,673,677,678,679,681,695,702,712,716,825,886,894,90
2,909,916,1101,1108,1109,1177,1187,1193,1204,1220,1239,1255,1256,1342,1347,1354,
1357,1362,1363,1364,1373,1375,1379,1403,1404,1405,1406,1413

Table 2a

List of informative probes for diagnosis of breast cancer

Clone ID	Sequence ID
I-24	308
I-28	310
I-30	1180
I-52	-
I-54	1181
II-41	397
II-70	424
II-87	441
III-06	458
III-20	1183
III-40	488
III-57	504
III-60	-
III-61	507
III-89	530
IV-14	684
IV-15	1185
IV-26	1186
IV-32	688
IV-41	-
IV-53	61
IV-62	-
IV-69	192
IV-80	701
IV-82	196
IX-10	736
IX-12	-
IX-38	757
IX-39	758
IX-42	-
IX-48	764
IX-77	785
V-11	1188
V-32	-
V-39	-
V-55	77
V-80	726
V-94	-
VI-07	93
VI-34	-
VI-41	-
VI-48	891
VI-49	-
VI-52	-
VI-55	897
VI-65	-
VI-70	108

Clone ID	Sequence ID
VI-72	-
VI-78	-
VI-84	-
VII-03	1196
VII-15	1199
VII-32	571
VII-39	576
VII-47	1200
VII-48	1201
VII-60	-
VII-73	601
VII-77	1203
VII-90	612
VIII-20	628
VIII-29	635
VIII-30	636
VIII-31	637
VIII-39	-
VIII-44	-
VIII-46	649
VIII-48	651
VIII-66	665
VIII-74	-
VIII-76	675
X-04	-
X-07	808
X-15	814
X-29	821
X-34	-
X-35	-
X-54	837
X-56	839
X-68	1207
X-72	849
X-94	860
XI-07	-
XI-13	1209
XI-50	-
XI-58	-
XI-81	1212
XII-07	1213
XII-17	-
XII-26	-
XII-27	-
XII-31	-
XII-32	-
XII-35	1214

Clone ID	Sequence ID
XII-36	-
XII-52	-
XII-59	1216
XIII-19	1219
XIII-29	-
XIII-52	939
XIII-62	-
XIII-84	-
XIII-92	1221
XV-18	-
XV-22	1099
XV-24	-
XV-25	1224
XV-28	-
XV-34	-
XV-42	-
XV-68	-
XV-74	-
XV-93	-
XV-94	-
XV-96	-
XVI-36	1056
XVI-53	1230
XVI-59	-
XVI-66	1074
XVI-76	1083
XVI-77	1084
XVII-07	-
XVII-08	-
XVII-17	-
XVII-28	-
XVII-29	-
XVII-31	1139
XVII-36	-
XVII-39	-
XVII-40	1231
XVII-48	1148
XVII-55	-
XVII-58	-
XVII-67	-
XVII-72	-
XVII-76	1160
XVII-82	-
XVII-87	1165
XVII-95	1172

Table 2b

List of sequences of probes informative for breast cancer

Please see the note at the bottom of Table 1. Some sequences are missing.

Clone ID	Sequence ID
I-13	1331
I-14	1178
I-24	308
I-25	309
I-28	310
I-30	1180
I-37	1440
I-42	1332
I-48	321
I-54	1181
I-60	327
I-72	1335
I-81	338
I-82	339
I-86	1336
I-88	1182
I-95	1337
II-02	360
II-03	361
II-06	364
II-07	365
II-10	368
II-21	378
II-23	380
II-24	381
II-25	382
II-27	384
II-33	390
II-34	391
II-41	397
II-42	398
II-46	401
II-47	1338
II-48	403
II-52	406
II-57	411
II-58	412
II-59	413
II-60	414
II-61	415
II-62	416
II-64	418

II-67	421
II-69	423
II-70	424
II-74	428
II-80	434
II-82	436
II-84	438
II-87	441
II-88	442
II-96	450
III-01	452
III-02	453
III-06	458
III-08	460
III-12	463
III-13	464
III-17	1344
III-18	469
III-20	1183
III-21	471
III-23	473
III-24	474
III-25	475
III-26	476
III-27	477
III-28	478
III-29	479
III-32	482
III-33	483
III-35	485
III-39	487
III-40	488
III-42	489
III-45	492
III-46	493
III-47	494
III-48	495
III-56	503
III-57	504
III-58	505
III-59	506
III-61	507
III-62	508
III-63	509
III-64	510
III-66	512
III-67	513
III-70	515
III-74	518
III-75	519
III-78	521

94

III-80	523
III-81	524
III-82	1348
III-85	526
III-86	527
III-88	529
III-89	530
III-92	1351
III-93	532
III-95	534
III-96	1352
IV-04	682
IV-13	683
IV-14	684
IV-15	1185
IV-17	685
IV-23	1353
IV-26	1186
IV-31	687
IV-32	688
IV-35	1355
IV-37	g6
IV-38	689
IV-42	691
IV-43	1239
IV-47	693
IV-53	61
IV-61	696
IV-64	697
IV-69	192
IV-72	699
IV-80	701
IV-82	196
IV-85	702
IV-93	1360
IV-96	705
IX-10	736
IX-12	738
IX-13	739
IX-24	747
IX-38	757
IX-39	758
IX-48	764
IX-50	766
IX-56	768
IX-62	773
IX-65	776
IX-72	782
IX-77	785
IX-91	796
IX-96	801

V-01	1361
V-03	706
V-04	707
V-07	708
V-08	709
V-11	1188
V-12	711
V-17	1364
V-24	714
V-25	1365
V-28	1189
V-35	1366
V-38	1190
V-39	1109
V-41	718
V-47	1368
V-49	1369
V-55	77
V-57	720
V-58	1370
V-61	721
V-64	722
V-65	1371
V-68	1448
V-71	1495
V-74	724
V-75	1372
V-80	726
V-90	1374
VI-03	864
VI-04	865
VI-07	93
VI-08	867
VI-09	1378
VI-12	869
VI-13	870
VI-14	871
VI-16	873
VI-19	875
VI-20	876
VI-21	1380
VI-23	878
VI-24	879
VI-25	1192
VI-26	881
VI-32	885
VI-39	887
VI-43	1382
VI-44	1193
VI-45	889
VI-48	891

VI-49	892
VI-50	893
VI-53	895
VI-55	897
VI-58	899
VI-66	903
VI-67	904
VI-70	108
VI-71	1387
VI-74	905
VI-75	906
VI-76	907
VI-77	110
VI-79	1389
VI-80	908
VI-85	910
VI-87	911
VI-88	912
VI-90	1390
VI-93	1391
VI-95	915
VI-96	1392
VII-02	1195
VII-03	1196
VII-06	1394
VII-08	1197
VII-09	1198
VII-10	1395
VII-11	1396
VII-15	1199
VII-17	560
VII-19	562
VII-21	564
VII-22	565
VII-23	566
VII-24	567
VII-25	1397
VII-26	250
VII-27	568
VII-29	570
VII-32	571
VII-33	572
VII-36	575
VII-39	576
VII-41	578
VII-42	579
VII-43	580
VII-46	583
VII-47	1200
VII-48	1201
VII-49	585

VII-54	589
VII-57	591
VII-58	592
VII-59	593
VII-62	594
VII-63	1202
VII-64	596
VII-66	598
VII-67	1399
VII-72	600
VII-73	601
VII-77	1203
VII-80	605
VII-82	607
VII-86	1453
VII-87	610
VII-90	612
VII-91	613
VII-92	614
VII-93	615
VII-96	617
VIII-09	618
VIII-10	619
VIII-13	622
VIII-16	624
VIII-20	628
VIII-21	629
VIII-22	1455
VIII-23	630
VIII-24	631
VIII-25	632
VIII-26	1456
VIII-27	633
VIII-28	634
VIII-29	635
VIII-30	636
VIII-31	637
VIII-32	638
VIII-33	639
VIII-34	1204
VIII-38	643
VIII-40	644
VIII-41	645
VIII-46	649
VIII-48	651
VIII-55	656
VIII-57	658
VIII-59	660
VIII-60	661
VIII-61	1205
VIII-64	663

VIII-66	665
VIII-73	672
VIII-74	673
VIII-76	675
VIII-80	679
X-07	808
X-15	814
X-20	817
X-29	821
X-34	825
X-46	833
X-54	837
X-56	839
X-68	1207
X-72	849
X-73	1208
X-94	860
XI-13	1209
XI-37	1460
XI-43	1210
XI-67	1211
XI-81	1212
XII-07	1213
XII-35	1214
XII-36	1215
XII-59	1216
XII-65	1028
XII-92	1217
XIII-03	917
XIII-04	1218
XIII-19	1219
XIII-24	926
XIII-51	938
XIII-52	939
XIII-67	947
XIII-69	949
XIII-88	1220
XIII-92	1221
XV-22	1099
XV-24	1101
XV-25	1224
XV-42	1108
XV-62	1226
XV-64	1118
XV-84	1125
XVI-19	1228
XVI-36	1056
XVI-53	1230
XVI-60	1071
XVI-66	1074
XVI-74	1081

XVI-76	1083
XVI-77	1084
XVII-31	1139
XVII-40	1231
XVII-48	1148
XVII-76	1160
XVII-87	1165
XVII-95	1172

Table 3

List of informative probes (Clone ID) selected for breast cancer diagnosis based on their occurrence criterion during variable selection.

Occurrence*	Clone ID
100%	XI-8,XVI-66,VIII-66,XVI-59,VII-03,XIII-19,XII-35,X-35,XI-50,XII-26,IV-53,XIII-29,XIII-62,I-30,III-06,XV-22,XV-94,VII-15,VII-39,IX-39,XVII-39,III-40,VII-32
90%	I-52,VI-65,VI-34,IV-62,XV-34,XVII-58,V-11,VI-78,XII-36,XIII-92,VIII-29,XVI-53,XVI-77,XI-13,XIII-84,IV-14,XII-31,V-80,VII-48,XVII-29,XVII-72
80%	III-60,VIII-74,IX-12,X-04,XIII-52,VIII-30,IX-38
70%	VI-49,X-29,VIII-48
60%	IV-82,IX-10,VI-52,X-68,VII-77
50%	IV-15
40%	XV-28,II-70,V-55
30%	XVII-17,XVII-67
20%	XI-58,XVI-36,VIII-39,VIII-44,III-61,IV-69,XV-68,X-72
10%	IX-42,IX-77,X-94,XV-96,XVII-55
5%	XII-59,XVI-76,I-54,XV-18,V-94,X-54,VI-07,VII-47,XVII-31,XVII-87,XVII-48
In at least one model	II-41,VI-41,III-57,III-89,VII-73,XV-25,IV-26,X-34,IV-41,VII-90,XV-42,XVII-82,XII-27,VIII-20,I-28,VII-60,VIII-76,III-20,VI-84,XI-07,XVII-28,XII-17,XVII-36,XII-52 ,XVII-76,VIII-46,VI-70,XV-74,XV-93,VIII-31,II-87,V-39 ,VI-55,X-07,X-15,XII-07,XVII-07,XVII-08,XVII-95,I-24,IV-32,V-32,VI-48,VI-72,IV-80,IX-48,X-56,XV-24,XII-32,XVII-40

*100% = Genes appearing in all the 75 cross validated models; 90% = Additional genes appearing in at least 68 out of 75 cross validated models; 5% = Additional genes appearing in at least 4 out of 75 cross validated models and so on.

Table 4q

List of informative probes for diagnosis of Alzheimer disease

Clone ID	Sequence ID		Clone ID	Sequence ID
I-01	-		III-60	-
I-02	-		III-63	509
I-13	-		III-68	-
I-21	-		III-74	518
I-34	313		III-80	523
I-37	-		III-82	-
I-42	-		III-85	526
I-58	326		III-92	-
I-71	-		III-96	-
I-72	-		IV-23	-
I-86	-		IV-26	-
I-95	-		IV-29	-
II-03	361		IV-31	687
II-05	363		IV-34	-
II-06	364		IV-35	-
II-10	368		IV-45	-
II-24	381		IV-80	701
II-25	382		IV-82	-
II-26	383		IV-93	-
II-33	390		V-01	-
II-34	391		V-02	-
II-42	398		V-03	706
II-47	-		V-04	707
II-57	411		V-06	-
II-61	415		V-07	708
II-69	423		V-12	711
II-75	429		V-15	-
II-83	-		V-17	-
II-84	438		V-21	-
II-88	442		V-25	-
II-90	-		V-35	-
II-94	448		V-42	-
III-02	453		V-43	-
III-05	-		V-47	-
III-06	458		V-49	-
III-08	460		V-52	-
III-10	-		V-54	-
III-13	464		V-58	-
III-15	-		V-59	-
III-17	-		V-65	-
III-23	473		V-68	-
III-26	476		V-71	-
III-35	485		V-75	-
III-39	487		V-79	-
III-43	490		V-80	726
III-44	491		V-90	-
III-53	500		V-91	-
III-56	503		V-92	-

Clone ID	Sequence ID
VI-02	-
VI-04	865
VI-09	-
VI-10	-
VI-12	869
VI-14	871
VI-17	-
VI-20	876
VI-21	-
VI-23	878
VI-41	-
VI-42	-
VI-43	-
VI-44	-
VI-48	891
VI-49	-
VI-50	893
VI-53	895
VI-71	-
VI-74	905
VI-76	907
VI-78	-
VI-79	-
VI-87	911
VI-88	912
VI-90	-
VI-93	-
VI-95	915
VI-96	-
VII-02	-
VII-03	-
VII-06	-
VII-10	-
VII-11	-
VII-19	562
VII-21	564
VII-25	-
VII-36	575
VII-42	579
VII-43	580
VII-46	583
VII-59	593
VII-63	595
VII-66	598
VII-67	-
VII-72	600
VII-73	601
VII-75	-
VI-02	-
VI-04	866
VI-09	-
VI-10	-
VI-12	873
VI-14	875
VI-17	-

Clone ID	Sequence ID
VII-91	613
VII-93	615
VIII-01	-
VIII-02	-
VIII-03	-
VIII-06	-
VIII-09	618
VIII-10	-
VIII-15	-
VIII-22	-
VIII-26	-
VIII-28	634
VIII-30	636
VIII-32	638
VIII-33	639
VIII-41	645
VIII-42	646
VIII-48	651
VIII-58	-
VIII-64	663
VIII-65	-
VIII-67	666
VIII-78	-
VIII-82	-
VIII-83	-
VIII-85	-
VIII-87	-
VIII-91	-
VIII-92	-
VIII-93	-
VIII-95	-

Table 4 b

List of sequences of probes informative for Alzheimer disease

Please see note to Table 1

Clone ID	Sequence ID
I-09	298
I-10	299
I-15	300
I-16	301
I-17	302
I-19	304
I-20	305
I-22	306
I-23	307
I-24	308
I-25	309
I-28	310
I-31	311
I-32	312
I-34	313
I-38	314
I-39	315
I-40	316
I-44	317
I-45	318
I-46	319
I-47	320
I-48	321
I-49	322
I-53	323
I-56	324
I-57	325
I-58	326
I-60	327
I-64	328
I-67	330
I-69	331
I-71	332
I-72	333
I-73	334
I-77	335
I-79	336
I-80	337
I-81	338
I-82	339
VI-02	340

VI-03	341
VI-04	342
VI-06	343
VI-07	344
VI-08	345
VI-09	346
VI-11	347
VI-18	348
VI-19	349
VI-20	350
VI-21	351
VI-22	352
VI-25	353
VI-26	354
VI-27	355
VI-31	356
VI-33	357
VI-35	358
VI-48	359
II-02	360
II-03	361
II-05	363
II-06	364
II-07	365
II-08	366
II-09	367
II-10	368
II-11	369
II-12	370
II-13	371
II-14	372
II-15	373
II-16	374
II-17	375
II-18	376
II-20	377
II-21	378
II-22	379
II-23	380
II-24	381
II-25	382
II-26	383
II-27	384
II-28	385
II-29	386
II-30	387
II-31	388
II-32	389
II-33	390
II-34	391
II-35	392

II-37	393
II-38	394
II-39	395
II-40	396
II-41	397
II-42	398
II-43	399
II-44	400
II-46	401
II-47	402
II-48	403
II-49	404
II-50	405
II-52	406
II-53	407
II-54	408
II-55	409
II-56	410
II-57	411
II-58	412
II-59	413
II-60	414
II-61	415
II-62	416
II-63	417
II-64	418
II-65	419
II-66	420
II-67	421
II-68	422
II-69	423
II-70	424
II-71	425
II-72	426
II-73	427
II-74	428
II-75	429
II-76	430
II-77	431
II-78	432
II-79	433
II-80	434
II-81	435
II-82	436
II-83	437
II-84	438
II-85	439
II-86	440
II-87	441
II-88	442
II-89	443

II-90	444
II-91	445
II-92	446
II-93	447
II-94	448
II-95	449
II-96	450
III-01	452
III-02	453
III-03	454
III-04	455
III-05	457
III-06	458
III-07	459
III-08	460
III-09	461
III-11	462
III-12	463
III-13	464
III-14	465
III-15	466
III-16	467
III-17	468
III-18	469
III-19	470
III-21	471
III-22	472
III-23	473
III-24	474
III-25	475
III-26	476
III-27	477
III-28	478
III-29	479
III-31	481
III-32	482
III-33	483
III-34	484
III-35	485
III-37	486
III-39	487
III-40	488
III-42	489
III-43	490
III-44	491
III-45	492
III-46	493
III-47	494
III-48	495
III-49	496
III-50	497

III-51	498
III-52	499
III-53	500
III-54	501
III-55	502
III-56	503
III-57	504
III-58	505
III-59	506
III-61	507
III-62	508
III-63	509
III-64	510
III-65	511
III-66	512
III-67	513
III-69	514
III-70	515
III-71	516
III-73	517
III-74	518
III-75	519
III-77	520
III-78	521
III-79	522
III-80	523
III-81	524
III-83	525
III-85	526
III-86	527
III-87	528
III-88	529
III-89	530
III-91	531
III-93	532
III-94	533
III-95	534
III-96	535
VII-02	547
VII-03	548
VII-04	549
VII-05	550
VII-06	551
VII-07	552
VII-08	553
VII-09	554
VII-10	555
VII-11	556
VII-12	557
VII-14	558
VII-15	559

VII-17	560
VII-18	561
VII-19	562
VII-20	563
VII-21	564
VII-22	565
VII-23	566
VII-24	567
VII-27	568
VII-28	569
VII-29	570
VII-32	571
VII-33	572
VII-34	573
VII-35	574
VII-36	575
VII-39	576
VII-40	577
VII-41	578
VII-42	579
VII-43	580
VII-44	581
VII-45	582
VII-46	583
VII-48	584
VII-49	585
VII-50	586
VII-52	587
VII-53	588
VII-54	589
VII-55	590
VII-57	591
VII-58	592
VII-59	593
VII-62	594
VII-63	595
VII-64	596
VII-65	597
VII-66	598
VII-71	599
VII-72	600
VII-73	601
VII-74	602
VII-76	603
VII-77	604
VII-80	605
VII-81	606
VII-82	607
VII-83	608
VII-84	609
VII-87	610

VII-89	611
VII-90	612
VII-91	613
VII-92	614
VII-93	615
VII-94	616
VII-96	617
VIII-09	618
VIII-10	619
VIII-11	620
VIII-12	621
VIII-13	622
VIII-15	623
VIII-16	624
VIII-17	625
VIII-18	626
VIII-19	627
VIII-20	628
VIII-21	629
VIII-23	630
VIII-24	631
VIII-25	632
VIII-28	634
VIII-29	635
VIII-30	636
VIII-31	637
VIII-32	638
VIII-33	639
VIII-34	640
VIII-36	641
VIII-37	642
VIII-38	643
VIII-40	644
VIII-41	645
VIII-42	646
VIII-43	647
VIII-45	648
VIII-46	649
VIII-47	650
VIII-48	651
VIII-50	652
VIII-51	653
VIII-53	654
VIII-54	655
VIII-55	656
VIII-56	657
VIII-57	658
VIII-58	659
VIII-59	660
VIII-60	661
VIII-61	662

VIII-64	663
VIII-65	664
VIII-66	665
VIII-67	666
VIII-68	667
VIII-69	668
VIII-70	669
VIII-71	670
VIII-72	671
VIII-73	672
VIII-74	673
VIII-75	674
VIII-76	675
VIII-77	676
VIII-78	677
VIII-79	678
VIII-80	679
IV-02	681
IV-04	682
IV-13	683
IV-14	684
IV-17	685
IV-28	686
IV-31	687
IV-32	688
IV-38	689
IV-40	690
IV-42	691
IV-44	692
IV-47	693
IV-55	694
IV-56	695
IV-61	696
IV-64	697
IV-65	698
IV-72	699
IV-73	700
IV-80	701
IV-85	702
IV-93	703
IV-95	704
IV-96	705
V-03	706
V-04	707
V-07	708
V-08	709
V-09	710
V-12	711
V-18	712
V-20	713
V-24	714

V-37	716
V-40	717
V-41	718
V-48	719
V-57	720
V-61	721
V-64	722
V-65	723
V-74	724
V-80	726
V-81	727
V-87	728
VI-13	870
VI-14	871
VI-16	873
VI-23	878
VI-24	879
VI-28	883
VI-32	885
VI-38	886
VI-39	887
VI-45	889
VI-46	890
VI-49	892
VI-50	893
VI-52	894
VI-53	895
VI-54	896
VI-55	897
VI-57	898
VI-58	899
VI-63	900
VI-65	902
VI-66	903
VI-67	904
VI-74	905
VI-75	906
VI-76	907
VI-80	908
VI-81	909
VI-85	910
VI-87	911
VI-88	912
VI-91	913
VI-94	914
VI-95	915
VI-96	916
I-13	1177
I-14	1178
I-30	1180

I-54	1181
I-88	1182
III-20	1183
IV-15	1185
IV-26	1186
IV-62	1187
V-11	1188
V-28	1189
V-38	1190
V-45	1191
VI-44	1193
VII-47	1200
I-42	1332
I-52	1333
I-86	1336
I-95	1337
III-10	1342
III-60	1347
III-82	1348
III-92	1351
IV-23	1353
IV-34	1354
IV-35	1355
IV-41	1356
IV-45	1357
IV-82	1359
V-01	1361
V-02	1362
V-06	1363
V-17	1364
V-25	1365
V-35	1366
V-42	1367
V-47	1368
V-49	1369
V-58	1370
V-75	1372
V-79	1373
V-90	1374
V-91	1375
V-94	1376
VI-10	1379
VI-41	1381
VI-43	1382
VI-71	1387
VI-72	1388
VI-79	1389
VI-90	1390
VI-93	1391
VII-25	1397
VII-60	1398

VII-67	1399
VIII-22	1403
VIII-26	1404
VIII-39	1405
VIII-44	1406
I-37	1440
V-32	1445
V-52	1447
V-68	1448
V-92	1449
VI-42	1450
VI-78	1452
VII-86	1453
VII-88	1454
IV-29	1490
V-15	1491
V-39	1492
V-54	1493
V-59	1494
V-71	1495

Table 5

Samples

Diagnosis	No. of women
Normal /Benign	42*
DCIS	3
Invasive cancer	26

* From one woman, whole blood was collected at weeks 1,2,3,4,5 following menstruation. Hence, the number of unique normal/benign samples tested in the experiment is 75

Information about women with breast cancer

Sample	AGE	Stage	Cancer type	Size hist. (mm)	Nodes
1	51	II	IDC	20	1/7
2	84	II	IDC	22	2/2
3	50	I	DCIS+ 1 IDC	>50 DCIS; 5 x 14	0/7
4	47	I	IDC	15	0
5	69	III	ILC g.2 + tubular adenocarcinoma	50 + 3	1 av 12 + 1 av 7
6	50	II	IDC	24	0
7	65	I	IDC	15	0
8	63	II	IDC	23	0
9	55	I	IDC + DCIS	4	0 av 1
10	52	0	DCIS + small colloid carcinoma foci	50 + 3	0
11	60	II	IDC	24	0
12	54	I	IDC	11	0
13		0	DCIS	20	0
14	49	0	DCIS	9	0
15	48	I	IDC	4	0
16	56	I	IDC	4	0
17	68	I	IDC	14	0
18	68	I	IDC	7	0
19	63	I	IDC	10	0
20	45	I	IDC	19	1
21	57	III	IDC	60	8/20
22	55	II	IDC/DCIS	35 +55	0
23	71	I	IDC/extensive DCIS	8	0
24	56	I	IDC	9	?

25	66	II	IDC	26	0
26	66	I	IDC	15	?
27	61	I	IDC	9	?
28	?	?	?	?	?
29	65	I	IDC	11	0

Other diseases /conditions present in the women tested

Other diseases /conditions present in the women tested

Disease/condition
Diabetes
Asthma
Ulcerous colitis
Hemochromatose
Crohn's disease
Fibromyalgia
Psoraiasis
Atopic eczema
Rheumatism
Allergies

Prior history of cancer in the women tested

Cancer type	No. of women
Breast	3
Colon	2
Stomach	1
Skin	1

Table 6

Number of samples tested by double cross validation and success of the diagnostic test for breast cancer based on selected informative genes

Number of samples tested by double cross validation

Number of unique samples tested	75
Number of unique non cancer samples tested	46
Number of cancer samples tested	29

Success of the diagnostic test for breast cancer based on selected informative genes

Occurrence in percentage[*]	Number of informative probes	Specificity	Sensitivity	Accuracy	False Positive rate	False negative rate	Total error rate
100.00	23	84.78	75.86	81.33	15.22	24.14	18.67
90.00	44	91.30	79.31	86.67	8.70	20.69	13.33
80.00	51	86.96	79.31	84.00	13.04	20.69	16.00
70.00	54	89.13	75.86	84.00	10.87	24.14	16.00
60.00	58	89.13	75.86	84.00	10.87	24.14	16.00
50.00	59	89.13	75.86	84.00	10.87	24.14	16.00
40.00	63	89.13	75.86	84.00	10.87	24.14	16.00
30.00	66	86.96	75.86	82.67	13.04	24.14	17.33
20.00	74	89.13	75.86	84.00	10.87	24.14	16.00
10.00	79	89.13	75.86	84.00	10.87	24.14	16.00
5.00	90	86.96	79.31	84.00	13.04	20.69	16.00
1.33	139	84.78	72.41	80.00	15.22	27.59	20.00

[*]100% = Genes appearing in all the 75 cross validated models; 90% = Genes appearing in at least 68 out of 75 cross validated models; 5% = Genes appearing in at least 4 out of 75 cross validated models; and so on.

Table 7

Double cross-validation and details of the success of the diagnostic test for Alzheimer disease based on the expression 182 informative genes

Success of diagnostic test

Performance	Description	%
Accuracy	Percentage of the total number of predictions that were correct	92.9
Sensitivity	Percentage of positive cases that were correctly identified	85.7
Specificity	Percentage of negatives cases that were correctly predicted	100
False positive rate	Percentage of negatives cases that were incorrectly classified as positive	0.0
False negative rate	Percentage of positives cases that were incorrectly classified as negative	14.3
Total error rate	Percentage of the total cases incorrectly predicted	7.1

Validation Result

Total number of samples tested	14
Number of Alzheimer's disease samples tested	7
Number of Alzheimer,s disease samples incorrectly predicted	1
Number of non_Alzheimer's disease samples tested	7
Number of non-Alzheimer's disease samples incorrectly predicted	0

Table 8

Some relevant features of the blood donors. B, Female donors with breast cancer; N, Female donors with suspected mammogram but no breast cancer; IDC, invasive ductal carcinoma; DCIS, ductal carcinoma in situ; na, not available nd, not determined; ++, no degradation of mRNA and no ribosomal contamination in the sample, +, no degradation of mRNA but ribosomal contamination in the sample.

		AGE	Cancer type /breast abnormality	Size Hist. (mm)	mRNA Quality
1	B1	na	IDC	5	++
2	B2	49	DCIS	8	nd
3	B3	54	IDC	18	++
4	B4	59	IDC	12	+
5	B5	61	DCIS+micro invasive cancer	15+1.5	++
6	B6	55	IDC	12+17	nd
7	B6		IDC	12+17	nd
8	N1	45	Fibroadenoma	-	nd
9	N2	52	na	-	+
10	N3	55	Cyst	-	++
11	N4	54	na	-	++
12	N5	51	Benign ductal epitelhelium	-	nd
13	N6	57	Benign	-	nd
14	N7	50	na	-	++
15	N8	52	na	-	+

Table 9

List of sequence of probes informative for both alzheimer and breast cancer disease

Clone ID	Sequence ID
I-24	308
I-25	309
I-28	310
I-48	321
I-60	327
I-72	333
I-81	338
I-82	339
II-02	360
II-03	361
II-06	364
II-07	365
II-10	368
II-21	378
II-23	380
II-24	381
II-25	382
II-27	384
II-33	390
II-34	391
II-41	397
II-42	398
II-46	401
II-47	402
II-48	403
II-52	406
II-57	411
II-58	412
II-59	413
II-60	414
II-61	415
II-62	416
II-64	418
II-67	421
II-69	423
II-70	424
II-74	428
II-80	434
II-82	436
II-84	438

II-87	441
II-88	442
II-96	450
III-01	452
III-02	453
III-06	458
III-08	460
III-12	463
III-13	464
III-17	468
III-18	469
III-21	471
III-23	473
III-24	474
III-25	475
III-26	476
III-27	477
III-28	478
III-29	479
III-32	482
III-33	483
III-35	485
III-39	487
III-40	488
III-42	489
III-45	492
III-46	493
III-47	494
III-48	495
III-56	503
III-57	504
III-58	505
III-59	506
III-61	507
III-62	508
III-63	509
III-64	510
III-66	512
III-67	513
III-70	515
III-74	518
III-75	519
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III-80	523
III-81	524
III-85	526
III-86	527
III-88	529
III-89	530
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III-95	534

III-96	535
IV-04	682
IV-13	683
IV-14	684
IV-17	685
IV-31	687
IV-32	688
IV-38	689
IV-42	691
IV-47	693
IV-61	696
IV-64	697
IV-72	699
IV-80	701
IV-85	702
IV-93	703
IV-96	705
V-03	706
V-04	707
V-07	708
V-08	709
V-12	711
V-24	714
V-41	718
V-57	720
V-61	721
V-64	722
V-65	723
V-74	724
V-80	726
VI-03	341
VI-04	342
VI-07	344
VI-08	345
VI-09	346
VI-12	869
VI-14	871
VI-19	349
VI-20	350
VI-21	351
VI-23	878
VI-25	353
VI-26	354
VI-48	359
VI-50	893
VI-53	895
VI-74	905
VI-76	907
VI-87	911
VI-88	912
VI-95	915

PCT/GB2003/005102

122

VII-02	547
VII-03	548
VII-06	551
VII-08	553
VII-09	554
VII-10	555
VII-11	556
VII-15	559
VII-17	560
VII-19	562
VII-21	564
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VII-24	567
VII-27	568
VII-29	570
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VII-96	617
VIII-09	618
VIII-10	619
VIII-13	622
VIII-16	624
VIII-20	628
VIII-21	629

VIII-23	630
VIII-24	631
VIII-25	632
VIII-28	634
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VIII-41	645
VIII-46	649
VIII-48	651
VIII-55	656
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VIII-59	660
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VIII-61	662
VIII-64	663
VIII-66	665
VIII-73	672
VIII-74	673
VIII-76	675
VIII-80	679

- 124 -

Nucleotide sequences

Sequence ID - 93   nt: 405
GGATCCTGTGGCCCACAGAGCTGCCCCAGCAGACGCTCCGCCCCACCCGGTGATGG
AGCCCCGGGGGGACAATCGTGCCTGGGGAGGAGCAGGGTACAGCCCATTCCCCCAG
CCCTGGCTGACCTGGCCTAGCAGTTTGGCCCTGCTGGCCTTAGCAGGGAGACAGGG
GAGCAAAGAACGCCAAGCCGGAGGCCCGAGGCCAGCCGGCCTCTCGAGAGCCAGAG
CAGCAGTTGAATGTAATGCTGGGGACAGGCATGCTGCCGCCAGTAGGGCGGGGACC
CGGACAGCCAGGTGACTACCAGTCCTGGGGACACACTCACCATAAACACATCCCCA
GGCAGGACAGATCGGGGAAGGGGTGTGTACCAGGCTATGATTTCTCTTGCATTAAA
ATGTATTATTATT

Sequence ID - 108   nt: 550
GGCTTTGACAGAGTGCAAGACGATGACTTGCAAAATGTCGCATCTGGAACGCAACA
TAGANACCATCATCAACACCTTCCACCAATACTCTGTGAAGCTGGGGCACCCAGAC
ACCCTGAACCAGGGGGAATTCAAAGAGCTGGTGCGAAAAGATCTGCAAAATTTTCT
CAAGAAGGAGAATAAGAATGAAAAGGTCATAGAACACATCATGGAGGACCTGGACA
CAAATGCAGACAAGCAGCTGAGCTTCGAGGAGTTCATCATGCTGATGGCGAGGCTA
ACCTGGGCCTCCCACGAGAAGATGCACGAGGGTGACGAGGGCCCTGGCCACCACCA
TAAGCCAGGCCTCGGGGAGGGCACCCCCTAAGACCACAGTGGCCAAGATCACAGTG
GCCACGGCCACGGCCACAGTCATGGTGGCCACGGCCACAGCCACTAATCAGGAGGC
CAGGCCACCCTGCCTNTACCCAACCAGGGCCCCGGGGCCTGTTATGTCAAACTGTC
TTGGCTGTGGGGCTAGGGGCTGGGGCCAAATAAAGTCTCTTTCTCC

Sequence ID 110
ACGAAGACAGACATCTGTGGAATGATTCACATCCTCTCAAGTTAGGAGGATGGAGG
CCTGCTTCATTAAGAAGCTGGGGGTAGGGTGGGGGTGGGGAGAACACTTAACAACA
TGGGGACCAGTCAGGGGAATCCCCTTATTTCTGTTTTGCATATGAGGAACCCTAGA
GCAGCCAGGTGAGGCTCTCTAGTTTAATAAAAATCATGGAAAGACTCTTAATGCAG
ACTCTTCTTAAGTGTTAATAGGGATTTTTTCAGCTTATTTTGGTTGCAGTTTCCAA
TTTTTAAAAATGTTGAGGTAATCTTTCCCACCTTCCCAAACCTAATTCTTGTAGAT
GCATTAGTGTTGAACCAATGCTTTCTCATGTCTCAATTCTTTGTATATGCATTCTT
TTCAGATGTATTAAACAAACAAAAACCCTTC

Sequence ID - 192   nt: 286
CCGGTAATAGAATAGAAAAGGGAGAGTGTCTTCATGCAATGTGGCATCCTGGATTG
GGTCTCGNNACAAAAACAGGACATTAGTGGGAAAATTGGAAATCTGAAAAAAGTCT

- 125 -

GAATTTTAGTTAATATACCAATTTCAGTCTCTTGGTTTTTGACAGATGTACCATGGT
GATGTAAGATGTTGACCTTGGGGTAGGCTGGGTGAAGGGTATACAGGAACTCTTTG
TACTATCTCTGCAACTTCTCTGTAAATCTAGTATCATTCCAAAATAAAAGTTTATT
TAATTT

Sequence ID 250
GTGGAAGTGACATCGTCTTTAAACCCTGCGTGGCAATCCCTGACGCACCGCCGTGA
TGCCCAGGGAAGACAGGGCGACCTGGAAGTCCAACTACTTCCTTAAGATCATCCAA
CTATTGGATGATTATCCGAAATGTTTCATTGTGGGAGCAGACAATGTGGGCTCCAA
GCAGATGCAGCAGATCCGCATGTCCCTTCGCGGGAAGGCTGTGGTGCTGATGGGCA
AGAACACCATGATGCGCAAGGCCATCCGAGGGCACCTGGAAAACAACCCAGCTCTG
GAGAAACTGCTGCCTCATATCCGGGGGAATGTGGGCTTTGTGTTCACCAAGGAGGA
CCTCACTGAGATCAGGGACATGTTGCTGGCCAATAAGGTGCCAGCTGCTGCCCGTG
CTGGTGCCATTGCCCCATGTGAAGTCACTGTGCCAGCCCAGAACACTGGTCTCGGG
CCCGAGAAGACCTCCTTTTTCCAGGCTTTAGGTATCACCACTAAAATCTCCAGGGG
CACCATTGAAATCCTGAGTGATGTGCACTGATCAAGACTGG

Sequence ID 299
CAGCGCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAG
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AGGTTTCTAAAACATGACGGAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATG
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AGGGCAATGCTTTTAGATTAAAATGAAGGTGACTTAAACAGCTTAAAGTTTAGTTT
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TAGGATGAAACAATTTTGGAGAAGATAGAAG

Sequence ID 300
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Sequence ID 302

AGTAGAGACGGGGTTTCACTGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGT
GATCCGGCCACCTCGGCCTCCCGAAAGTGCTGGGATTACAGGCGTGAGCCACGGCG
CCCAGCCCCAGCCTGTCACTTAAACTGATAAACGACAGATTAACAGTAGAAAAATT
5   TTATTTTGCATACATAATGAGGCTTCACAAAAGAGAAGTGAAAACCCAAGTAGGAG
TTTAGGGCTGGGGGCTTATATACCATTTAACAAGGGGTGATAAATTGTAAGAGAAT
AG

Sequence ID 304
10   TCCTTGGTTTCGATTTGTGGCAACAATCCAGTCTTTTTGTTTTTTTCAGGGATACC
ATATGTAACAGGTGCCATTGTTACTGTAACTTTTCACACATGCCTTCAGTTTGATG
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CTTTACTTTTAGAAAGTCTTATCTTTTATGCCACAGAAATAGCATTTGGCTATTAG
TCATGGATGGCAAAGAAATTAATTTTGAGTTGTTTGGATAAAAATGTTTCAGTTGA
15   CTGTAGTGTGTATTGAGAGACACTGCCAGTAAACAAACTCTCTTGGTAGGTGGAAA
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20   TCAAGTTGCTTATCTGAAATCTTTATGAATCAACACTAGTCACTAAGTCTAGCTCG
ACC

Sequence ID 306
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25   TGTGAGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCTC
GACATTCGGGAAGTGTTTTTGAGAAGTCTCGGTCGGTAAGGGAAGTCTTCCAAGTC
CGTGCAGCACTAACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCCAGATGAGG
CAGCTGTGACTGTGTCAAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTT
CCACTGCCGTCTCCACAGGAAACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCAT
30   CAAGGCATTTATTGCAGTGTACTATTTGCTTCCAAAGGATCAGGCCCTGAGAACAA
TGACCTTATTTCCTACAACAGTGTCTGGGTTGCGTGCCAGCAGATGCCTCAGATAC
CAAGAGATAACAAAGCTGCAGCTCTTTTGATGCTGACCAAGAATGTGGATTTTGTG
AAGGATGCNCATGAANAAATGGACNAGCTGTG

35   Sequence ID - 308   nt: 373
AAGTGGGTCTTGCCATCCCTGAACTGNAATCATCCCTAACATATTCATACCTGTTT
TCATTTTAAAAGTTGGGTCAGTTTTTTTATTAGTACATGTATTTCTATCCTACTGA

TTTATTTGCTATATCATCTAATTTAGTTTGAATATTCCATAATTTACTTAATTAGT
CCTGTATGGAGACCTAGCTCTTCTCAGTGTCTACTATTATAAACAATGCTACAGTG
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TATTGCTAAACCAGAAGATAACCTGCATTTAAAATTTGACTGCTAGGGNCAGGGNC
5   ACATTTAATTAAATTAGAACAANGAATGCATAATGNC

Sequence ID 309
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GTTCTAGGCAATCTGAAGGAAACCAGAAAATGTGAATTTCTCTTCCCTCAAAAAGC
10   TATACTGAAGTAGTATTTAATATTCAAGTACTTGTAAATTTGCAGAACAGTACTTT
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AAACCATCTAAAAGATTTCTGGTTTATTTCTCCAACTCCTAATAAATAGGGTCAC
ATATTTTTTAACTTTTTTCTAATTTGAAAAGTAATACAGGCATATGGTATTTTAAA
AATGAAACAACACAAAGGGATATGTTTTGAAAAGTGGTCTTGCCATCCCTGAACTG
15   TAATCATCCCTAACATATTCATACCTGTTTTCATTTTAAAAGTTGGGTCAGTTTTT
TTATTAGTACATGTATTTCTATCCTACTGATTTATTTGCTATATCATCTAATTTAG
TTTGAATATTCCATAATTTACTTAATTAGTCCTGTATGGAGACCTAGCTCTTCTCA
GTGTCTACTATTATAAACAATGCTACAGTGAATATTGGTGNATAAATCCTACACAC
CACGTAACATATCTTAAGTTCCTGGAAGAGATATTGCTAAACCAGAAGATAACCTG
20   CATTTAAAATTTGACTGCTAGGGTCAGGGTCACATTTAAATTAAATTAGAACAAGG
AATGCATAATGTCTTCGATAGCAATCTATTCAAGGTGCACCGTGGTCACAAAGGAA
AGCAAAACTGTC

Sequence ID - 310 nt:564
25   CCTGGNCAGAGGCCTCTATCCTGTANTGATAATTGCCATCAAAATTGTCAAAAANG
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TTTTTGTGTGGGAATGGGGTTGGATAAACCAATGAACTTTATTATAAACAAATCCC
ACCTATATCTANCAAATTTATATTTTCGGTGAAATACAGATATTTGCCTTTCTGGA
GTANTATAGAAGCTGTCAATATGTATCTACTGTACAGTACTAAATAGTATTCATTT
30   ATGAAATGAGTAGTGTTTGGGTGGCTGGGGTTAAGGAAAAATGAGACTTGGAATTG
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AAAAACTGAAATGCCATATAGAAAAACAGCATTGTTTTTACAGTTTGTAGTAAGTA
ACTTTTTAAAGATTTTATCAAAAAGAATTTTGTCTATNGTGAGTAAAAGAAGTTCT
AATAATGGCCTAATCACTGCATTTTTAAAAAACAAAGTTCAACACAAATGACATTT
35   GTTT

Sequence ID 311

- 128 -

CCTCTCCTCCATCTAAAGGCAACATTCCTTACCCATTAGTCTCAGAAATTGTCTTA
AGCAACAGCCCCAAATGCTGGCTGCCCCCGGCCAAGCATTGGGGCCGCCATCCTGC
CTGGCACTGGCTGATGGGCACCTCTGTTGGTTCCATCAGCCAGAGCTCTGCCAAAG
GCCCCGCAGTCCCTCTCCCAGGAGGACCCTAGAGGCAATTAAATGATGTCCTGTTC
5   CATTGG

Sequence ID - 313   nt: 554
CCCGGAATCGCGGCCCGCGTCGACAACAAACCTGCATGTTCTGCACATGTATCCAG
GAACTTAAAAAAAAAAAAGATAGTTTGTGTGTCTTAATTGAATAATAGTAGATTT
10   ATAGATTAAAGATCTATGGGTTTTTAATATGGATTANAAATCTGTGGGTTTTTGAT
ATGGATTANAAATCTGTGGGTTTTTAATATGGATTGGAAATCTGTGGGTTTTTAAT
ATGGATTAAAAACATCTGTGGGTTTTTAATATGGATTAAACATCTGTGGGTTTTT
AATATGGATTAAACATCTGGGTTTTTAATATGGATTAAACATCTGTGGGTTTTTAA
TATGGGTTAAAAATCAAAGAAAATGAACTATTTGCTCCAGTGCAGGAAAATACAG
15   GCAATACTGGATACAATTAGATGGTCAGGAGCGATAACCCGGTTGCCATTGTTTGA
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AGGGGGAGTCTTCTATGTAGTTAGTGAAGGCTAAATGAACTATTATATGC

Sequence ID 314
20   CTTTTCCTCCCGCTGTCCCCCACGGAGGGGACTGCTCTCCCCGCTGCATCCTTTC
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GACATTCGGGAAGTGTTTTTGAGAAGTCTCGGTCGGTAAGGGAAGTCTTCCAAGTC
CGTGCAGCACTAACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCCAGATGAGG
CAGCTGTGACTGTGTCAAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTT
25   CCACTGCCGTCTCCACAGGAAACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCAT
CAAGGCATTTATTGCAGTGTACTATTTGCTTCCAAAGGATCAGGCCCTGAGAACAA
TGACCTTATTTCCTACAACAGTGTCTGGGTTGCGTGCCAGCAGATGCCTCAGATAC
CAAGAGATAACAAAGCTGCAGCTCTTTTGATGCTGACCAAGAATGTGGATTTTGTG
AAGGATGCACATGAAGAAATGGAGCAGGCTGTGGAAGAATGTGACCCTTACTCTGG
30   CCTCTTGAATGATACTGAGGAGAACAACTCTGACAACCACAATCATGAGG

Sequence ID 315
TGGTACAGATACAAACTGGACTCTCAGGACAAAACGACACCAGCCAAACCAGCAGC
CCCTCAGCATCCAGCAGCATGAGCGGAGGCATTTTCCTTTTCTTCGTGGCCAATGC
35   CATAATCCACCTCTTCTGCTTCAGTTGAGGTGACACGTCTCAGCCTTAGCCCTGTG
CCCCCTGAAACAGCTGCCACCATCACTCGCAAGAGAATCCCCTCCATCTTTGGGAG
GGGTTGATGCCAGACATCACCAGGTTGTAGAAGTTGACAGGCAGTGCCATGGGGGC

AACAGCCAAAATAGGGGGGTAATGATGTACGGGCCAAGCACTGCCCAGCTGGGGGT
CAATAAAGTTACCCTTGTACTTG

Sequence ID 316
CGCCACTTATCCAGTGAACCACTATCACGAAAAAAACTCTACCTCTCTATACTAAT
CTCCCTACAAATCTCCTTAATTATAACATTCACAGCCACAGAACTAATCATATTAA
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Sequence ID 321
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TTTAGCCAAGAAGCAAACCATCTAAAAAGATTTCTGGTTTATTTCTCCAACTCCTA
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TATGGTATTTTAAAAATGAAACAACACAAAGGGATATGTTTTGAAAAGTGGTTCTT
GCCATCCCTGAACTGTAATCATCCCTAACATATTCATACCTGTTTTCATTTTAAAA
GTTGGGTCAGTTTTTTTATTAGTACATGTATTTCTATCCTACTGATTTATTTGCTA
TATCATCTAATTTAGTTTGAATATTCCATAATTTACTTAATTAGTCCTGTATGGAG
ACCTAGCTCTTCTCAGTGTCTACTATTATAAACAATGCTACAGTGAATATTGGTGT
ATAAATCCATACACACCACGTAACATATCTTAAGTTCCTGGAAGAGATATTGCTAA
ACCAGAAGATAACCTGCATTTAAAATTTTGACTGCTAGGGTCAGGGTCACATTTAA
ATTAAATTAGAACAAGGAATGCATAATGTCTTCGATAGCAATCTATTCCAGGTGCA
CCGTGGTCACAAAGGAAAGCAAAACTGTCAATAACTTTCTTCTCA

Sequence ID 322
TAGCATTTGGCCTTTTAAAACATTTGTTTATTTTTTTTCTGAGAATGGCTAACACA
CTTTATTGAGGTTCGAAATTAATAAAGAAAATAAAAGAAATGTATCTTCATTCATT
CTGTATGTTAGTGTTTTAATTACCCTTAGAATATATGGATAAAAAATACTATTCTT
TGTCTTGGAGAAGGTAAGAGTCTAGTTAGATGAATAAGGGTTATCTATGTAGAACA
ACTAGAGAATGAGAAGAGAGCTTATGAGATTGAGTACTACGTTATGCAGTAGAGTA
GCACGTCATCTGCTACTGAGTATGGTGTGATAACATTGTGTAACAGGAAAGTATGA
TCAATATCTACTTAAAATTAAGGACAATATTAGCACTACATTGCTTTATTTTAAAG
TAAAAATTAGAGAACTAAACACAAGCATTGTAAGTACAATAAAAGCTGATCTTTCT
AGTTAAGCAGAATAATACATGTTCAAGCATCTGCTAAATCATTAAATATAAGAATA
TAGGGGTTTTCTATAATCTTATTTTCTTTGGAAGAGTACCTCATTTTCAAGANGAG
AAGTTTCTAATTGCCACTTCTTTAAAAATAAACAGGGTTTTAATGTTCCCAGCAC
AAAAATTAATATCTCTTCAAAAAGTCTCTTGTGATTAAGTTTGAATCCCTTGTCAT
ACTGCTTCTAATATTGACACTGACCTCCTTAGGTATTTTTCAGGGGTTATAATCTT
TTCTTAAGGTATCTTTTTTCAAGAATTGGATACCTTGGGCTT

Sequence ID 323
CGCGTCGACTTTTAAAGTCATCTCTATAGGAAGGTGCTGGGCAGGGATCCCAGAGA
AAGAAAGGGTCCAAGACTCCATTAACTGCCCTGGATGAAGGGCACTGCTACAGCAG
CTAGTACCAGAGACTCTCCTATCTCACGGTTGAGGCAGACCCAGGATAGAATAGAG
5   AATAAAAGGAATGCTTATAGGAAACAATTTTGTATGGAATGCTAGATGGCCAAGCC
TCAGCCTTTGGTCCAGTGCAACCCTTGCCTCGCTTGTCAACAGTGAAAAATTAGTT
TGGTTAGAAGAACCATCTGGAAACACACCAGCTTCTGCTACCTTCATGCTCATTGT
TAAAAAAGATTAACCAGTGTGAACATTCTGATCTGTTAATTCCAGGGACTGTTTT
CTTTCCAATGGACTGTTTGTTGGTAGAATAACCCCCAAAAGCTCAAAGCTAAAATG
10   CATCATCAGTCCTAGTCGGCAGTTCCTTAAGAATGGACTGGCGGCGTGGTTGAGCT
GATATGGAAAGCTGCACCTTCCTGCAGAAGATCAACTGACCTGCTATCCCACCCC
AAATTCAACCTGAGGTATATTTCAGTGAAGCAGGTAGCTGTGCTTCTCAAAGCAGA
GAAGCAGTTTTAAGAACCAAAAAGGTAGAGGAAATCTA

15   Sequence ID 324
GTTTGTTACAGGCAGAATTGGATAGATACAGCCCTACAAATGTATATGCCCTCCCC
TGAAAAAAATTGGATGAAAATCTGCACAGCAAAGTGAAACACACAGATAATAGGAA
CAAAATGTAGTTCCCATGTGCCAAACAAAATAAATGAAATCTCTGCATGTTTGCAG
CATATCTGCCTTTTGGGAATGTAATCAAGGNATAATCTTTGGCTAGTGTTATGTGC
20   CTGTATTTTTTTAAAATGGTACACCAGAAAAGGACTGGCAGTCTACTTCTACCATA
GTTAAACTTCACCCTCTTTAATTTCACAACATATTCTTTGGAAGCAGGAAGAAATG
CTCATAAAGAGGATCAGACCTTCTTTCCCGTGAAACCAGTATTTGGCGCCATATAT
AAGCCTGGTTAAATTGGTCATCTAAAGCTGTCAAATAAGACATTCTGTGAAAGGTA
AACATCGAAACTGGTTATAAGTAAAACCATCAAGCCAACAACAGGGTCTTGAGATA
25   ACCTTTGAAGCTTATTGTCTGGCCTGCACCAGAAGATGTCTGCATTACTCATTGCT
AAAAATGTGTACACAGAACTGCACTAGGATTAATTGGTTCAAGAAGAAATTTAAAC
TTACGTTTGGGTTTCCATACAGCACTCTATTGAATACATGCATCTGAATTTAAGTT
GCAA

30   Sequence ID 325
GACCAGTAATGGCTTTTAAGAGTCCATTTTGTCATTGTCTCCCTAGTTAATTACAG
GTGGGGGATCTTTTGCCTCTATTCTCTTCATATTGAAATGAATCATACTCATGTTT
TGTGGAACTCCTTAAAGTTGTAGCTGTCATGATCAGATTTTTTTTATATTTCCTCA
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35   AGTGACACATAATCTTATCTCTTTATAGAACCTTAAATTTTATCATTATTTTCGCT
TAGAATACAGCATTTCTTTGCTTCTGTTGCTGGTTTGACTTAAGAAATAAGGCAGT
AACTCTGATCAATCAATTATCCATAAGGAAGGGCTTTTCATGGGTTCTATTAATTT

- 131 -

GTTAGTACCCTAAGTATATCTGAAAAATATGTCTATTGAGAGAAGATTTTGGCATT
CCAGATGGTATAGTCTATATATATTTAAAGTTTTGAATTTGCTTATATATACTCAG
CTTTCTTTTTCTAGCATTTTTGCATTTACCTGTTAATTGAAGTATACCCCCCACAT
ATAAAGTTCCTCTTAAAGACACTGGACTCTTTCTGGGGGGCTAAAATA

Sequence ID - 326   nt: 554
CCCGGAATCGCGGCCCGCGTCGACAACAAACCTGCATGTTCTGCACATGTATCCAG
GAACTTAAAAAAAAAAAAAGATAGTTTGTGTGTCTTAATTGAATAATAGTAGATTT
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AATATGGATTAAACATCTGGGTTTTTAATATGGATTAAACATCTGTGGGTTTTTAA
TATGGGTTAAAAATCAAAGAAATGAACTATTTGCTCCAGTGCAGGAAAATACAG
GCAATACTGGATACAATTAGATGGTCAGGAGCGATAACCCGGTTGCCATTGTTTGA
AGAAGAGAATAAGGNGCTAGCATTCCTATCCGTAGATAATTTGACAGCTAGGAAAT
AGGGGGAGTCTTCTATGTAGTTAGTGAAGGCTAAATGAACTATTATATGC

Sequence ID 327
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TTGAGGACTTCTGGAGGATGATCTGGGAGGGGAAGTCCCACACTATCGTGATGCTG
ACGGAGGTGCAGGAGAGAGAGCAGGATAAATGCTACCAGTATTGGCCAACCGAGGG
CTCAGTTACTCATGGAGAAATAACGATTGAGATAAAGAATGATACCCTTTCAGAAG
CCATCAGTATACGAGACTTTCTGGTCACTCTCAATCAGCCCCAGGCCCGCCAGGAG
GAGCAGGTCCGAGTAGTGCGCCAGTTTCACTTCCACGGCTGGCCTGAGATCGGGAT
TCCCGCCGAGGGCAAAGGCATGATTGACCTCATCGCAGCCGTGCAGAAGCANCAGC
AGCAGACAGGCAACCACCCATCACCGTGCACTGCAGTGCCGGAGCTGGGCGAACA
GGTACATTCATAGCCCTCAGCAACATTTTGGAGCGAGTAAAAGCCGAGGGACTTTT
ANATGTATTTCAAGCTGTGAAGAGTTTACGACTTCAGAGACCACATATGGTGCAAC
CCTGGAACAGTATGAAATGTGCTACAAAGTGGTACAAGATTTATTGATATATTTCT
GATTATGCTAATTTCAATGAAGATCCTGCCTTAAATATTTTTTAATTTAATGGCAN
AT

Sequence ID 328
CAAGACTCCATCTCAAAAAAAAAAAAAAAATCTACAGTGCTGAGTATATAAAATTAT
TAACACATTTCACAACAATATGTGTTTGTGGAGTTAAATATTTTTTGTCTTTAAAA
CAGGTAATTTTAGTGCATACTTAATTTGATGATTAAATATGGTAGAATTAAGCATT
TTAAATGTTAATGTTTGTTACATTGTTCAAGAAATAAGTAGAAATATATTCCTTTG

- 132 -

TTTTTTATTTAAATTTTTGTTCCTCTGTAAACTAAAAGAACACGAAGTAATTGGTC
ACAATTACTGGTGTTTAACTGCCAAATATGGGTAAATAAGGGAAAATTTTGTTTAA
TATTTAGTCCTTCTGAGATGGCTTGAATATTTGAATTTTGTTGTACGTCTATACTG
GGTAGTCACAAGTCTTATAAACACTTTAGAGGAAAGATGGATTTCAGTCTGTATTT
5   TTAAACATCATTTATTTTAAATCTGGTGCTGAAAAATAAGAAAAAAATTAAACTGC
ATTCTGCTGTTCTTCTTTANAAGCATTCCTGCGTAAATACTGCTGTAATACTGTCA
TGCAAAGTGTATCCTTTCTTGTCGTATCCTTTTTGGGGCAGTGGTTTTT

Sequence ID 330
10   GCGGGAATCGCGGCCCGCGTCGACCTCAAAGGAGAAAAAAAACCTTGTAAAAAAAG
CAAAAATGACAACAGAAAAACAATCTTATTCCGAGCATTCCAGTAACTTTTTTGTG
TATGTACTTAGCTGTACTATAAGTAGTTGGTTTGTATGAGATGGTTAAAAAGGCCA
AAGATAAAAGGTTTCTTTTTTTTTCCTTTTTTGTCTATGAAGTTGCTGTTTATTTT
TTTTGGCCTGTTTGATGTATGTGTGAAACAATGTTGTCCAACAATAAACAGGAATT
15   TTATTTTGCTGAGTTGTTCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAATTTTAAAATTTTTAAAATAAAACCCTTGGTTAT

Sequence ID 331
GCCGCGTCGACCTGCATGAGCCACAGTTTCTTGACTGGAGGCCATCAACCCTCTTG
20   GTTGAGGCCTTGTTCTGAGCCCTGACATGTGCTTGGGCACTGGTGGGCCTGGGCTT
CTGAGGTGGCCTCCTGCCCTGATCAGGGACCCTCCCCGCTTTCCTGGGCCTCTCAG
TTGAACAAAGCAGCAAAACAAAGGCAGTTTTATATGAAAGATTANAAGCCTGGAAT
AATCAGGCTTTTTAAATGATGTAATTCCCACTGTAATAGCATAGGGATTTTGGAAG
CAGCTGCTGGTGGCTTGGGACATCANTGGGGCCAAGGGTTCTCTGTCCCTGGTTCA
25   ACTGTGATTTGGCTTTCCCGTGTCTTTCCTGGTGATGCCTTGTTTGGGGTTCTGTG
GGTTTGGGTGGGAAGAGGGCCATCTGCCTGAATGTAACCTGCTAGCTCTCCGAAGC
CCTGCGGGCCTGGCTTGTGTGAGCGTGTGGACAGTGGTGGCCGCGCTGTGCCTGCT
CGTGTTGCCTACATGTCCCTGGCTTGTTGAGGCGCTGCTTCAACCTGCACCCCTCC
TTGTCTCATAGATGCTCCTTTTGACCTTTTCAAAATTAATATGGATGGGAAAGCTC
30   CTATGCCTTTTGGCTTCCTGGTAGAAGGCGGGATGCCCAAGGGTCTGCCTGGGTGT
GGATTGGATGCTTGGGGTGTGGGGGTTGGAAACTGTCTTGTGGCCCACTTGGGCCC
C

Sequence ID 335
35   CCCGCGTCGACTTTTAAAGTCATCTCTATAGGAAGGTGCTGGGCAGGGATCCCAGA
GAAAGAAAGGGTCCAAGACTCCATTAACTGCCCTGGATGAAGGGCACTGCTACAGC
AGCTAGTACCAGAGACTCTCCTATCTCACGGTTGAGGCAGACCCAGGATAGAATAG

- 133 -

AGAATAAAAGGAATGCTTATAGGAAACAATTTTGTATGGAATGCTAGATGGCCAAG
CCTCAGCCTTTGGTCCAGTGCAACCCTTGCCTCGCTTGTCAACAGTGAAAAATTAG
TTTGGTTAGAAGAACCATCTGGAAACACACCAGCTTCTGCTACCTTCATGCTCATT
GTTAAAAAAGATTAACCAGTGTGAACATTCTGATCTGTTAATTCCAGGGACTGTT
5   TTCTTTCCAATGGACTGTTTGTTGGTAGAATAACCCCCAAAAGCTCAAAGCTAAAA
TGCATCATCAGTCCTAGTCGGCAGTTCCTTAAGAATGGACTGGCGGCGTGGGTGAG
CTGATTTGGAAAACTGCCCTTCTGCAAAAAACACTGGCCTGCTTTCCA

Sequence ID 337
10   CAAGACTCCATCTCAAAAAAAAAAAAAAATCTACAGTGCTGAGTATATAAAATTAT
TAACACATTTCACAACAATATGTGTTTGTGGAGTTAAATATTTTTTGTCTTTAAAA
CAGGTAATTTTAGTGCATACTTAATTTGATGATTAAATATGGTAGAATTAAGCATT
TTAAATGTTAATGTTTGTTACATTGTTCAAGAAATAAGTAGAAATATATTCCTTTG
TTTTTTATTTAAATTTTTGTTCCTCTGTAAACTAAAAGAACACGAAGTAATTGGTC
15   ACAATTACTGGTGTTTAACTGCCAAATATGGGTAAATAAGGGAAAATTTTGTTTAA
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GGTAGTCACAAGTCTTATAAACACTTTAGAGGAAAGATGGATTTCAGTCTGTATTT
TTAAACATCATTTATTTTAAATCTGGTGCTGAAAAATAAGAAAAAAATTAAACTGC
ATTCTGCTGTTCTTCTTTAGAAGCATTCCTGCGTAAATACTGCTGTAATACTGTCA
20   TGCAAAGTGTATCCTTTCTTGTCGTATCCTTTTTGGGGCAGTGGTT

Sequence ID 338
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AGAGGATACCATATGTGGGTGCCGGGGGGGATAGGTGAGAAGTACTAGAAGGCGGA
25   ATGGAAGGACACTTCTGCTCAGCTCTGTGACACGGGCAGGGACCCTGCAGGGCTCA
GGTCCTTTAACACAGCAGCTTCATTCTAACACCAGCAGCGTTGGAACACACGTACA
AGTATGCAGACTAAGCTCTTGCTTGGCTGATACGGCTTTTTGGGTTTTTAGAGAAC
ATGCATATATGTTCTCATTCATGGTACATGAACTCAGAAGCCTTACTGCCTATTTT
TGTTAATACTTCTGGGCAAACATTACCACTTACAACTCACACCAGTTAGAAATCAT
30   TTGTAAAATGTTATTTAATAAAGCCAAAGAACTAAATCATATTTATTTTCCAAGGN
TTTCTAAGATCTCTGAAACTAATGAGGTTTTTTAAATCCCCATTAAGTACTCATCA
CTGCTAGTAAAAGCAGTTGTCTTTACCTTTAATTCCAGTGAGTCCCCTTAAATTTA
TTTTTTATTATCTTTGGCTACATTGCCTTAGACAAAATGTGGTCACCCTAATTTAA
NGGATAAAATTCACATCCTCACAGATTTCTTATTAAGAGGGTCTAANCCTTGAATA
35   ATCANCAGTGGAAATGGAAGTCTTCTTTACTGGNTTTNATCCTTTCCCTTTTTTAT
CCCATG

Sequence ID 339

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TTTTTTTTTAAATAAAGCTGTCGGCACTCAAGGGTAATTTCATATCAGTGTGNTCT
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GCATAAAGGTTTAAAGATATCACAAAGATGCCAAGTGATTAATAATGTTTTAAACC
ACCCCTTTTTCTGTCTGAAAAAACAACTAAAACAATATTACAACAGTATAGTTACA
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ATATATATACTTTTGAGGGGGTGGCTAATGCAGAAACACCCAAGACCTAAGGAAGA
TACAACCCCATTTCTAGGTGTGAGGTCTAAATGCTTCACACACCCACTTGTGACCT
TTTTTCATGAAGAATCATAACACTGTGCAGTGAGAAACAGTGGCAAAGCAATACTG
AAAGCATTTTAAATTATTTACTAGGTTAAAAGGGTGAACTGATACTTTAAATACAT
CAAATTTCATCAT
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10

Sequence ID 360

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GCAAGTGAGAGCCGGACGGGCACTGGGCGACTCTGTGCCTCGCTGAGGAAAAATAA
CTAAACATGGGCAAAGGAGATCCTAAGAAGCCGAGAGGCAAAATGTCATCATATGC
ATTTTTTGTGCAAACTTGTCGGGAGGAGCATAAGAAGAAGCACCCAGATGCTTCAG
TCAACTTCTCAGAGTTTTCTAAGAAGTGCTCAGAGAGGTGGAAGACCATGTCTGCT
AAAGAGAAAGGAAAATTTGAAGATATGGCAAAAGCGGACAAGGCCCGTTATGAAAG
AGAAATGAAAACCTATATCCCTCCCAAAGGGGAGACAAAAAAGAAGTTCAAGGATC
CCAATGCACCCAAGAGGCCTCCTTCGGCCTTCTTCCTCTTCTGCTCTGAGTATCGC
CCAAAAATCAAAGGAGAACATCCTGGCCTGTCCATTGGTGATGTTGCGAAGAAACT
GGGAGAGATGTGGAATAACACTGCTGCAGATGACAAGCAGCCTTATGAAAAGAAGG
CTGCGAAGCTGAAGGAAAAATACGAAAGGTA
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15

20

Sequence ID - 361   nt: 622

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GTGCACCTNTCTGAGAAACATANNAGACAATGAGGAAAAGGATTCANCATTCCGTG
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CAAAGATTTGTTTTTAATGTCTAATTAATAAAATTTTAAAGGAAGAAACATTCTAA
TACTTTAATTATAAAAGTTAACTATTTTCAAAGGTATCAAAATACAGTTAAACCT
TTAAAATGTATATTTCTTAATATCTTGAAATTGTAATGCCTTTTTTTTTTCCTAAA
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ACTTTGTCCCTGCCTCCCATCCCTGGATATCANGTTTGTGGATATCTACAGTTAAT
AGAGTGACCAAATAGTAGGAATACTGTCTCTCTATTCTGAATAAAATACTTTGAAT
CAGATTTAGAAATAATGAATAAAATACAAATCACCATTGAAATTGCTCTAATTTTG
AGAGCT
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25

30

35

- 135 -

Sequence ID - 363   nt: 628
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AAGATCGTGCCACTGCACTCCAGCCTGTGTGACAGAACAAGACTCTGTCTCAAAAA
AAAATAATAATAATAATAATAAAAAGGAATAACATAGCTAGGAATAAATTTAA
TCAAAGAGGTGAAAGACTTATACACTTAAAACTACAAAAAAAAATCACTGAAGGA
ATTATAGACCCAAATAAAAATAAATAAAAAGACATTCTGTGTTTTAGGGAAAGAAG
ACTTAATATTGTTAAGATGTCAATACTACCCAAAGTGATCTACAGATTCAACATAA
TCCCTATCAAAATTCCAACAGCCTACTTTGTAGAAATGGAAAAGCCAATTTTCAAA
TTCAGATGGAATTGCGAGGGGTTCTGAATAACAAAAACAATCTTGGGGAAAAAAAA
CAAAAAACAAAGTCAAAGAACTCACACTTCTCTATTTATAAATTTACTACAAAGTT
ATAGTAATCAAA

Sequence ID - 364   nt: 528
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ATGTAGAGCATTCATCACCCACCATTCATTCACTGCCTACTCCCACCACAGCTGTT
TCGTGGTCTGTCTGCTCCCTGTGCCACCCCCACCCCATCAGGTGGGCCTTTTGCAA
GTGATGAAGTCACCTGTGGGGGAAGAGCTTTCCTTTCCTCTCCTCAACTCAGAAGG
CCTCTTCCTCTTGCTCAAGAGGGTGCTGCTGCTTTCTGCCTCCTTCCCCGGCCGGC
CTCCATCCCAGTTCACCTTTTCAGAAATGGCCCCTCAGTCAACTCTTCCCTTTTCT
CCTGGCTTTTTATTTCTCCCAGTCTCTTAAGAGTATCCTTAGCTTTAAAAACAATA
ACACAGAGGATGGGTGCAGTGGCTCATGCCTGTAATCCCAGCACTTTGGAGCCTGG
GGCGGGCGGATCACTTGAGGNCA

Sequence ID 365
GTCCCGGAATCGCGGCCGCGTCGACCTTTTCTATGCCTGCTATATAAACAGTACCT
TGCAAGATGTCCTGTCTGATATCCACAAAGGGGTATTGTCAACCCCAAGTTCAGAC
AGCTTTGTATTCTTCTGTCCCTGGATACATGAATTACTGCCATCTTTACACAGCGC
CCTAAAATACCAACGCGAAGTTACCTGCTCAGCTTGAAGCTGCGCTGTACCCTGGA
ACCAGCACTTCTGCTGAATGACTCAGGATGAAGCCTCGACTTCTCCTTCCCATCCC
ATGCCCAGACCCCAGTGGCTCCTTTCCCAATCTGATCCAGTGACTTTAAGTCCAGC
TGTTGCAACCTGGGCATGAGGAGGAGTGCAAGATGGCTTTGTCCTACCTGGAAAGA
GGCTTTCTGGA

Sequence ID 366

- 136 -

CACCATTTACACACAGTGGGTCCTTGAATAGCATCGTTTTATTCAATGTCATTTTG
TTATAACATTGAGAAAAAATTGATTCCCGGCTGGGGCCACTGTCTGTGCACCGT

Sequence ID - 368   nt: 329
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GCAAATTCAAAAGCTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAGCTGAA
AGAGATAGAGACACAAAAAACCATTCAAAAAAAAACAATGAATCCAGGAGTTTTTT
TTTTAAAAAGATCAACAGAATTGACAGACTGCTAGCAAGACTAATAAAGAAGAGAG
AAGCATCAAATAGACTCAATAAAAAATGATAAAGGGGATATCACCACCAATCCCAC
AGAAATACAAACTACCATCAGAGAACACTATAAACACCTCTATGCAAAT

Sequence ID 369
GAAAGATCTAAAATCGACACCCTAACATCACAATTAAAAGAACTAGAGAAGCAAGA
GCAAATTCAAAAGCTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAGCTGAA
AGAGATAGAGACACAAAAAACCATTCAAAAAAAAACAATGAATCCAGGAGTTTTTT
TTTTAAAAAGATCAACAGAATTGACAGACTGCTAGCAAGACTAATAAAGAAGAGAG
AAGCATCAAATAGACTCAATAAAAAATGATAAAGGGGATATCACCACCAATCCCAC
AGAAATACAAACTACCATCAGAGAACACTATAAACACCTCTATGCAAATAAACTAG
AAAAT

Sequence ID 370
GAAAGATCTAAAATCGACACCCTAACATCACAATTAAAAGAACTAGAGAAGCAAGA
GCAAATTCAAAAGCTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAGCTGAA
AGAGATAGAGACACAAAAAACCATTCAAAAAAAAACAATGAATCCAGGAGTTTTTT
TTTTAAAAAGATCAACA

Sequence ID 371
GCCCGGAATCGCGGCCGCGTCGACGTAAGCTCGGCTGAATCCACGGTTCAAGAACA
GGAAAGAAGGCCAAGGCATAGGGAGTGGGGCAGTTGGGTGAATATTAGTACCTTTC
CCTCAGNTNCATTAATTACCCCTGCCTACTCTGCACAAAAGGATNTAACAACAGTT
TCCTTTTTAATGGCCAGGTACAGCTGCTTATATGGANGGGCATTTNTNAATGATAT
CCTTNATCACTGTCTTAATCATCACATNCTTAAAACAATCACTTTATTGTGTTAAG
GAAGATAAAAATGGCTGGGTTCAATTTCCGTTCTGGAAGAAATCGANTNAAAAGGT
AACCATTTAATAATGCANAGGGCANTTTCACTGCAGACCCTAATACTGGAAATTTT
TAAAAACAAATGAAAACTTCTACTTTTTCTTCTAAGCTTACTTAACCACCCAAAT
TTTCCAGCCACATATCTTCCTAGTCTACAACTGCCTTTAACTTTAAGAGATGCTCA
AAAAAATGTAAATTCTCAAATACATTCTTATTACAATTACTGCTAACCT

Sequence ID 373
CCAGTGTGCTGGGATTACAGGCATGAGCCCTGCACCCAGCCTCTTAAACTGATCAT
ATGATATTGGTTCTCAACCAAGGGTGACTTTGCCCCCAGAGGATACTTGGCAATGT
CTGGAGATACTCAGTTGTCATGACTTGGACAGGTGCTACTGTCACCCAGTGGGTAG
AGGTCAGGGATGGTGCTAAACATAGGACAGCTGTCAAGAGAAAAGAATGTACCCAG
CCCCAAATGTCAGTAGGGCTGAGGTTGAGAAACCCAGCTGTAGCTGACGTGTGAAG
GACAGACTGGCCTGGAAGTGTGTTTTCTGCCCCTTTCCACCCCTGCATATTAGTTA
AGGCCAAAGGAAAAAAGGAATGCAGGAAATGCCCGTTAAAAATCTTCAAAACAATA
TAAAATGATCAATTCCACTAAAACCCTTTACACATTTAAGTATAAAGGTATTGGTA
GGAAAATTTGTTATTCACTGCTTTTCTCAGTGTCATGAAATAATTATTTCTGCTGT
CAGTTT

Sequence ID 374
AAAAAAAAAATCACTGAAGGAATTATAGACCCAAATAAAAATAAATAAAAGACAT
TCTGTGTTTTAGGGAAAGAAGACTTAATATTGTTAAGATGTCAATACTACCCAAAG
TGATCTACAGATTCAACATAATCCCTATCAAAATTCCAACAGCCTACTTTGTAGAA
ATGGAAAAGCCAATTTTCAAATTCAGATGGAATTGCGAGGGGTTCTGAATAACAAA
AACAATCTTGGGGAAAAAAACAAAAACAAAGTCAAAGAACTCACACTTCTCTAT
TTATAATTTACTACAAAGTTATAGTAATCAAAGTCGACGCGGCCGCGATTCCGGG

Sequence ID 378
CGACTGCGGCTCTTCCTCGGGCAGCGGAAGCGGCGCGGCGGTCGGAGAAGTGGCCT
AAAACTTCGGCGTTGGGTGAAAGAAAATGGCCCGAACCAAGCAGACTGCTCGTAAG
TCCACCGGTGGGAAAGCCCCCCGCAAACAGCTGGCCACGAAAGCCGCCAGGAAAAG
CGCTCCCTCTACCGGCGGGGTGAAGAAGCCTCATCGCTACAGGCCCGGGACCGTGG
CGCTTCGAGAGATTCGTCGTTATCAGAAGTCGACCGAGCTGCTCATCCGGAAGCTG
CCCTTCCAGAGGTTGGTGAGGGANATCGCCCAGG

Sequence ID 380
GCAATTTAATTTTTAATAACAAAGATACTGTATTTTAACATGGTGAAATATACTTG
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TTGTACAGAACATTCCATAGATCAACAGAAAATACATTTGAGCGCAAAAATAAAAA
ATATTTAAGGAGAATCTCTAAGCAGCATTTTATTTCTGCAAAAGACATATCTTGTC
TGATTAAATATCTACAAGTGCTTTTCCTTTCAAAAATACATATATTCTTAATAGAC
TAAGTCATTAACAATGACCTGGTAATTCTTTCACTTCAATTTGAATGATTTATAAG
CTAAATCTTCAACCACAAAAAGGTTTTTATTTGTATTAAGATGTTACCACTTTTGA

- 138 -

CAAAAAGCTTAAAATATTTTATATTTCAAAGGAAAATTAGCAACATAACTTTACAA
TATATTCTATGATATTTTGATTGTGAGGGCTACTCTATTTAAAACTGATGATCTCT
GTTGTGTTGCTCAGATGCAGGAAAGCAGCAAAA

Sequence ID - 381   nt: 534
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ATCTTCTCAGTCATGAGGTAATCTGGTGACTACCCTTCCTCAAAGCCAGTTGGGAT
ATTCTTTGAATAGAGTAAAACAGTGTTTCTAGGCTGGGAGACACCAGACATAGTTG
AGGACAGAGGTGCTAGAAAATAGGAAGTTTAAAAGCATGTGCGGTGATGCTCAGAG
GAGGTAAACCCCACCCTCATGCTCATAGCTTCCAATCATTTTCTCTAGTTCTTAAC
TCTTAAATGTGAGAAATGCTTGAAGATTCTAGTCATCTGAAGAAAGTCTCTTTATT
AAAGATTTTCATAAAAGAGACCAAAGCAGACAAACAGAAAAAGACATCTTGGGGAA
AAAAACAAGGATAATGGGAAGAGAAGGAAAGTTTTAAAAATTATCAATATCCTCAG
GGGGACAAAATATTATATCCTATAAAGACAGATTTTTATTTTTTAAAAAAATAGAA
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Sequence ID - 382   nt: 444
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ACGCTGCTTGAGGCTCTGGACTGCATCCTACCACCAACTCGTCCAACTGACAAGCC
CTTGCGCCTGCCTCTCCAGGATGTCTACAAAATTGGTGGTATTGGTACTGTTCCTG
TTGGCCGAGTGGAGACTGGTGTTCTCAAACCCGGTATGGTGGTCACCTTTGCTCCA
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AGCTTTTCCTGGGGACAATGTGGGCTTCAATGTCAAGAATGTGTCTGTCAAG

Sequence ID - 383   nt: 566
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ATCAAGAAACCAGACTGTGATGACTGGGAGAGCGGGCTGAATGCAATGGAGTGTGC
ATTACATTTGGAAAAAAATGTGAATCAGTCACTACTGGAACTGCACAAACTGGCCA
CTGACAAAAATGACCCCCATTTGTGTGACTTCATTGAGACACATTACCTGAATGAG
CAGGTGAAAGCCATCAAAGAATTGGGTGACCACGTGACCAACTTGCGCAAGATGGG
AGCGCCCGAATCTGGCTTGGCGGAATATCTCTTTGACAAGCACACCCTGGGAGACA
GTGATAATGAAAGCTAAGCCTCGGGCTAATTTCCCCATAGCCGTGGGGTGACTTCC
CTGGTCACCAAGGCAGTGCATGCATGTTGGGGTTTCCTTTACCTTTTCTATAAGTT
GTACCAAAACATCCACTTAAGTTCTTTGATTTGTCCATTCCTTCAAATAAAGAAAT

- 139 -

TTGGTA

Sequence ID 384
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GCTCACATCTGTAACCCTAGCACTCTGGGAGGCTGAGGTGGGTGGATCATGAAGTC
AAGAGATAGAGACCATCCTGGCAAAAATTAGCTGGGCGTGGTGGGGTGCGCCCGTA
GTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATTGCTTGAGCCCGGGAGGCGGAG
GTTTCATTGAGCCGAGATAGTGCCACTGCACTCCAGCCTGGACAACAGAGCGAGAC
TGTGTCTT

Sequence ID 386
CTAAGGGTTTAAAGATGGAAAGAGGCATTGATGAACAGCTGGGGAAGGAGTAGTTT
GAGGTAGATGTGCAGATGGAATGAAGAGAAGGTCTCAAGAAGAGGGTGGAGCCAAA
GAGGGCTGCAGATTTAGAAGGCTAAAGTCTTTAGATGGCTTTGGATAGCCTGTTGT
ATCTTGGACCATGCAGGTTACAGTGGAGCATGGAGTGGGGACAGAAGTGGAGGAAG
GAACCAGGGAACATGGAGTGAGAAGCTAAAGGAAAGTGATGCAGTAGATACATGGC
TCTAAAGTACTCAGGACTTTCAGAGGCTTAAACATAGGGTGACCAACTATCCCACT
ATGCCTGATACTAAGGGCATTCCCTGGATGTGGACCTTTCATTCCCCAAATTAGGA
AAGTCTTGGGCATACCAAGACAAGTTGGCCACCCTACTCAAAAGTATGTAAGCTAA
CATATCTGTTCTCTAAGAGGTTAAAGCTGGATGGGGATACCAGATGTATGTACGTG
ATGCAGTTAAACAGCAATACAAGGGGGCAAGTCTACCTGATCGGCCAATTCAATGG
GA

Sequence ID 387
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GAGAAAATCAGTGGTTTAAGAAGTTAGAATAATGATTATCTTTGGAGGGATTGCAA
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TGAGTGCCGACTACATGAGTGGTTAGGTTTGCAAAATTCATTGAGTTATGCACTTA
ATGGTGTTGTCTTATTAGAGCTGATGGAGGAGAGAGGGCTTCAATTTGCACAACTG
AGTAATCAGCTAGGCCCAGTCACTAGGTGAACAACTTACTGCTCCAATCAGCCTTA
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TTCCTTCAGAGTCACTCTTGAATAGCTGAAATAGTAAATGTTAAATCTGTGGATGC
AAGTGTGTAAATTATTTTAGTCATCAGCTCTAATAAGATGGCCTTTGGGGAAATGA
GTATAAGGTCACGAAAATGAAATGGCAAGAAGGAGGTCTACTATTTCTTCTGTAAT
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CTTTTTCTTTAATAA

Sequence ID 388
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AAAAATCCCAAACATATAACTGAACTCCTCACACCCAATTGGACCAATCTATCACC
CTATAGAAGAACTAATGTTAGTATAAGTAACATGAAAACATTCTCCTCCGCATAAG
CCTGCGTCAGATTAAAACACTGAACTGACAATTAACAGCCAATATCTACAATCAA
CCAACAAGTCATTATTACCCTCACTGTCAACCCAACACAGGCATGCTCATAAGGAA
AGGTTAAAAAAGTAAAAGGAACTCGGCAAATCTTACCCCGCCTGTTTACCAAAAA
CATCACCTCTAGCATCACCAGTATTAGAGGCACCGCCTGCCCAGTGACACATGTTT
AACGGCCGCGGTACCCTAACCGTGCAAAGGTAGCATAATCACTTGTTCCTTAATTA
GGGACCTGTATGAATGGCTCCACGAGGGTTCAGCTGTCTCTTACTTTTAACCAGTG
AAATTGACCTGCCCGTGAAGAGGCGGGCATAACACAGCAAGACGAGAAGACCCTAT
GGAGCTTTAATTTATTAATGCAAACAGTCCTAACAAACCCCAGGTCCTAAACTCCA
AACCTGCATTAAA

Sequence ID 389
CGACCCGGAATTCGCGGCCGCGTCGACTGAGTTCTTGACAAGAGTGTTTTTCCCTT
CCCGTCACAGAGTGGGCCCAACGACCTACGGCACTTTGACCCCGAGTTTACCGAAG
AGCCTGTCCCCAACTCCATTGGCAAGTCCCCTGACAGCGTCCTCGTCACAGCCAGC
GTCAAGGAAGCTGCCGAGGCTTTCCTAGGCTTTTCCTATGCGCCTCCCACGGACTC
TTTCCTCTGAACCCTGTTAGGGCTTGGTTTTAAAGGATTTTATGTGTGTTTCCGAA
TGTTTTAGTTAGCCTTTTGGTGGAGCCGCCAGCTGACAGGACATCTTACAAGAGAA
TTTGCACATCTCTGGAAGCTTAGCAATCTTATTGCACACTGTTCGCTGGAAGCTTT
TTGAAGAGCACATTCTCCTCAGTGAGCTCATGAGGTTTTCATTTTTATTCTTCCTT
CCAACGTGGTGCTATCTCTGAAACGAGCGTTAGAGTGCCGCCTTAGACGGAGGCAG
GAGTTTCGTTAGAAAGCGGACGCTGTTCT

Sequence ID - 390   nt: 523
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ACAAAGAACTGGAAAGTGAAAAAGAGCAACTTAAGAAGGGTTTGGAGCTCCTGAAA
GCATCTTTCAAGAAAACAGAACGCTTAGAAGTTAGCTACCAGGGTTTAGATATAGA
AAATCAAAGACTGCAAAAAACTTTAGAGAACAGCAATAAAAAATCCAGCAATTAG
AGAGTGAACTACAAGACTTAGAGATGGAAAATCAAACATTGCAGAAAAACCTAGAA
GAACTAAAAATATCTAGCAAAAGACTAGAACAGCTGGAAAAAGAAAATAAATCATT

- 141 -

AGAGCAAGAGACTTCTCAACTGGAAAAGGATAAGAAACAATTGGAGAAGGAAAATA
AGAGACTCCGACANCAAGCAGAAATTAAAGATCCACATTTGAAGAAAATAATGTGA
AGATTGGAAATTTGGAAAA

5   Sequence ID - 391   nt: 566
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ATCAAGAAACCAGACTGTGATGACTGGGAGAGCGGGCTGAATGCAATGGAGTGTGC
ATTACATTTGGAAAAAATGTGAATCAGTCACTACTGGAACTGCACAAACTGGCCA
10   CTGACAAAATGACCCCCATTTGTGTGACTTCATTGAGACACATTACCTGAATGAG
CAGGTGAAAGCCATCAAAGAATTGGGTGACCACGTGACCAACTTGCGCAAGATGGG
AGCGCCCGAATCTGGCTTGGCGGAATATCTCTTTGACAAGCACACCCTGGGAGACA
GTGATAATGAAAGCTAAGCCTCGGGCTAATTTCCCCATAGCCGTGGGGTGACTTCC
CTGGTCACCAAGGCAGTGCATGCATGTTGGGGTTTCCTTTACCTTTTTCTATAAGTT
15   GTACCAAAACATCCACTTAAGTTCTTTGATTTGTCCATTCCTTCAAATAAAGAAAT
TTGGTA

Sequence ID 394
GACCCGGAATCGCGGCCGCGTCGACCATTTTAGCCAAGGTGCCTCTATAGGGGTCA
20   AGACATCATGTGCCCAGACCTAAGGTCAGGAATGTCATATTTTTCTGTTAAAATCA
TTTTATTTCTGTGTATCTTACCTTTAAATCATTGTGGTTTACTCTGAGATTCTGTA
GTCCTAATATTGTATCATTGTGCTGTCTGCAAAACAACTTGAATCTATTTTGTTTG
CATCTTTTGTTACATGTAACGCAGCTGTACTTTATGTTCTTTGCAACTGTTTCCAT
TATGAACGCTGTGCTATTTACAAGGTTACATTTTTCTTGGCCAGGCGAGGTGGT
25   CATGCCTGTGATCCCAGCACTTTGGGAGGCCAAGGTGGGCGGATCACTTGAGGTAA
AGAGTTGAGACCAGCCTGGCTAGCATGGCGAAGCCCAGTCTCTACTAAAAATACAA
AAATTGGCCGGGTGAAATTAGCCGGGCGTGGTGGTGTGTGCTTGTAATCCCAGCTA
CTCGGGAGGCTGAGGCAGGAGAATCGCTTGAATCCGGGAGGCAGAGGTTGCAGTGA
GCCAAGATCANGCCACTGCACTCCACCTCGGGGTCAAGAGCGAAACTCTGTCTCAA
30

Sequence ID 395
CCGTTTTAGTCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCTGCCTCGGCC
TCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCGTAAATCAGGTTT
TTTAAATGTTTGCCAAACCTTATCACTGACTTTTATAACAAAATTATTTACTATAA
35   TCATTAGGGAATATTTAAGTTCTGCTAATACTTAAAATTGCAGAGTGCTAAAACCA
GCAGTGAGTTTAGAATCAAGCTAAGCTTTATTGTTGCTACTATTTGAGGCATATTA
GTTGACTGGTGTTCATATGCAAGGCAGTCTACTGGGTGCAACAAGGGTTAGAAGGA

- 142 -

TATTTTTAAAAAACTGACCCTATTCTCAGGATGAAAATAATACACTAGTAATAGTC
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GGGAAGGAGAGGAAGAATCATATTCCTTCACTAGCAGGATCAAGAAAGCTTTTATA
GAAATATACAAATCTTCACTTCTTGAAGGATTGGTAAAATTTAATAGCCAACATT
5   GGGCACTTATTCATTCTCTGAGTAAATATTTATTGCAT

Sequence ID 396
CTTAAATCTAAATGGACCACATTCTCTACTTAAAAAAATGCTATTAACCATGTGAT
CTTCTCAGTCATGAGGTAATCTGGTGACTACCCTTCCTCAAAGCCAGTTGGGATAT
10 TCTTTGAATAGAGTAAAACAGTGTTTCTAGGCTGGGAGACACCAGACATAGTTGAG
GACAGAGGTGCTAGAAAATAGGAAGTTTAAAAGCATGTGCGGTGATGCTCAGAGGA
GGTAAACCCCACCCTCATGCTCATAGCTTCCAATCATTTTCTCTAGTTCTTAACTC
TTAAATGTGAGAAATGCTTGAAGATTACTAGTCATCTGAAGAAAGTCTCTTTATTA
AAGATTTTCATAAAGAGACCAAAGCAGACAAACAGAAAAAGACATCTTGGGGAAA
15 AAAACAAGGATAATGGGAAGAGAAGGAAAGTTTTAAAAATTATCAATATCCTCAGG
GGGACAAAATATTATATCCTATAAGACAGATTTTTATTTTTTAAAAAAATAGAAA
GCAAACAAGCTCCTAAAAA

Sequence ID - 397   nt: 534
20 GACCCGGAATCGCGGCCGCGTCGACGGAAGCTCCTGCCCCTCCTAAAGCTGAAGCC
AAAGCGAAGGCTTTAAAGGCCAAGAAGGCAGTGTTGAAAGGTGTCCACAGCCACAA
AAAGAAGGAGATCCGCACGTCACCCACCTTCCGGCGGCCGAAGACACTGCGACTCC
GGAGACAGCCCAAATATCCTCGGAAGAGCGCTCCCAGGAGAAACAAGCTTGACCAC
TATGCTATCATCAAGTTTCCGCTGACCACTGAGTCTGCCATGAAGAAGATAGAAGA
25 CAACAACACACTTGTGTTCATTGTGGATGTTAAAGCCAACAAGCACCAGATTAAAC
AGGCTGTGAAGAAGCTGTATGACATTGATGTGGCCAAGGTCAACACCCTGATTCGG
CCTGATGGAGAGAAGAAGGCATATGTTCGACTGGCTCCTGATTACGATGCTTTGGA
TGTTGCCAACAAAATTGGGATCATTTAAACTGAGTCCAGCTGCCTAATTCTGAATA
TATATATATATATATCTTTTCACCATAA
30

Sequence ID - 398   nt: 512
GGGGAGCCCCCTCTTCCCTCAGTTGTTCCTACTCAGACTGTTGCACTCTAAACCTA
GGGAGGTTGAAGAATGAGACCCTTAGGTTTTAACACGAATCCTGACACCACCATCT
ATAGGGTCCCAACTTGGTTATTGTAGGCAACCTTCCCTCTCTCCTTGGTGAAGAAC
35 ATCCCAAGCCAGAAGAAGTTAACTACAGTGTTTTCCTTTGCACCGATCCCCACCC
CAATTCAATCCCGGAAGGGACTTACTTAGGAAACCCTTCTTTACTAGATATCCTGG
CCCCCTGGGCTTGTGAACACCTCCTAGCCACATCACTACAGTACAGTGAGTGACCC

- 143 -

CAGCCTCCTGCCTACCCCAAGATGCCCCTCCCCACCCTGACCGTGCTAACTGTGTG
TACATATATATTCTACATATATGTATATTAAAACTGCACTGCCATGTCTGCCCTTT
TTTGTGGTGTCTAGCATTAACTTATTGTCTAGGCCAAAGCGGGGGTGGGAGGGGAA
TGCCACAG

Sequence ID 399
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TTTTTCTTCCAAGATTAATTTGAATTTTTTTATGGACATTAGAAAACATTGCAGTT
TAGTCATAATCAAAAATAAATCTTGAGGCTGGTAGAGCAGCTTTGTTGCTGTTTAT
ATTTTTATTGCTTACTGGATTTCAGTGTTACCTAGTGCCATCAGTTTGGTATTTTG
CCACCTTGCACATTCAGTGATGTTTGATTTTTCTTTTTTCCTTTTTTTTCATATTACT
TTTAAATCCTGAATAGTTTGTGGCAGCTGGAGATCACCTAGTCCACCACTGTCCAA
CATGGCAATGGTAAGTAATATTGAGTAAAGAATAGAAAATTAGTAAAATGCATGGC
TTCAGAATTATAGCAATTTGCAAAATAGGTTAATGGATGAAAATTAGAATGACCAG
TTTAACTTTCCCCCCAGCAGATTCTTCTGTTAAACAATGCCCCTTCAAAATAAAGG
AAGAACAAGTGGGTGTTATACCTATGTTATTTGGCTATGTTAGCACAATATGATGG
ACTAATTTGAGAAAAGCATTTACTTCCTTTACTATTACTTCTTTTCTTTATAGGG
CTAAGTCTGCCTTCTGGGTCTTTGAA

Sequence ID 400
GAAGAAGCGCGAAGAGCCGTTAGTCATGCCGGTGTGGTGGCGGCGGCGGAGACTGC
GGGCCCGTAGCTGGGCTCTGCGAGGTGCAAGAAAGCCTTTGAGGTGAAGGTGTATG
AAAGTCATCATAACAGATGTTTTCCAAAAACTTGTAGAAGGTTGTGAAAAAACTAC
TAGGATCACGCGGCATGTATTGAGCATATAGGTTGCTGTAGATGAATGTTCTTAGC
TGTCATGTTTAAAAATACTTCTGCTTCGTTACCTCAAGTGTGGCATGCAGCATTTT
GGAAGGAAAATTGAAGACGTGTTCAAGAAAACATGAACAGAAGCAAATGATGAAAA
TGAGCATTTTACTTGATGTTGATAACATCACAATAAATTATGGAGAAAAATACATA
TTTGGCTAACTTTTAATTGCTGAACAATAAAGTGTTTTCTTTTAAATCNAAAAA

Sequence ID 401
GAAGCCAAACCAAAGGGAGCTTCTACTTCATGATGCCATTTATGTAAAGTTCAGGC
AGAGAAAATCAGTGGTTTAAGAAGTTAGAATAATGATTATCTTTGGAGGGATTGCA
ACTGGAAGAAGTCATGATTGGGATTTCTGGGTCCTAATAGTGCTCTGTGTCTTGAT
CTGAGTGCCGACTACATGAGTGGTTAGGTTTGCAAAATTCATTGAGTTATGCACTT
AATGGTGTTGTCTTATTAGAGCTGATGGAGGAGAGAGGGCTTCAATTTGCACAACT
GAGTAATCAGCTAGGCCCAGTCACTAGGTGAACAACTTACTGCTACCAATCAGCCT
TAGAGCAGGAATCAAACTCATGTCTCAGAAAAGTTATTAATTCAGCTTGTCTTGGG

ACTTCCTTCAGAGTCACTCTTGAATAGCTGAAATAGTAAATGTTAAATCTGTGGAT
GCAAGTGTGTAAATTATTTTAGTCATCAGCTCTAATAAGATGGCCTTTGGGGAAAT
GAGTATAAGGTCACGAAAATGAAATGGCAAGAAGGAGGTCTACTATTTCTTCTGTA
ATACTGATTTTTACCCCATCAGGGTCAGTCCCCAAAGGTTGTAAATGTGAAGCTTG
5   GTCTTTTTCTTTA

Sequence ID 402
GACCCTATTCTCAGGATGAAAATAATACACTAGTAATAGTCTGCTCTGTTGGTTAA
CTCCTCGTAAGGAGGTACAATTAAAATGCTGTAGTGTTGCAAGGGAAGGAGAGGAA
10   GAATCATATTCCTTCACTAGCAGGATCAAGAAAGCTTTTATAGAAATATACAAAAT
CTTCACTTCTTGAAGGATTGGTAAAATTTAATAGCCAACATTGGGCACTTATTCAT
TCTCTGAGTAAATATTTATTGCATGCTTATCTTGTATCAACATTGNGATGAAAGCN
CAAGAATGAAAGAGGAGGGAGAATGTTTANAGAATAAGGCTGAAACACAGATTTTG
TAGGGAGCGTAGGGGAGACTGANAAAACAG

15

Sequence ID 403
AAGACACCTGATAGATTGTCTTGTATTATTTTTCCTTTGCCTTCTTACAATCTCAG
TGATTAGAATTGGGCTGAAAACAATACATCAAATTCTCAGCAAAATCCTTATGGGT
TGCTGGATACCGAGGGTTTTTAAGATCTTTAGACTTCACTATATAGAACAAATGTT
20   GAATGGGAATTTTCTTTATTTCTATANCGTTTNG

Sequence ID 405
CCCGGAATCGCGGCCGCGTCGACGATGAGCATTTTTTCATGTGTCTTTTGGCTGCA
TAAATGTCTTCTTTTGAGAAGTGTCGGTTCATATCCTTTGCCCACTTTTTGATGGG
25   GTTGTTTTTTTCTTGTAAATTTGTTTGAGTTCATTGTAGATTCTGGATATTAGCCC
TTTGTCAGATGAGTAGGTTGCGAAAATTTTCTCCCATTTTGTAGGTTGCCTGTTCA
CTCTGATGGTAGTTTCATTTGCTGTGCAGAAGCTCTTTAGTTTAATTAGATCCCAT
TTGTCAATTTTGGCTTTTGTTGCCATTGCTTTTGGTGTTTTAGACTTGAAGTCCTT
GCCCATGCCTATGTCCTGAATGGTAATGCCTAGGTTTTCTTCTAGGGTTTTGATGG
30   TTTTAGGTCTAACGTTTCAGTCTTTAATCCATCTTTTAAAAGTCTCTTCACAGTAC
ATGAGTAGTAGTGACACCAATAATGTCAGAGCAGGGAACTCCCAGGTTCTGCCCAT
CCACAAAAACAACAAATAAGCTGGCAAAAACTTTAAGAATCAACTTTTGCAGATCT
CTGAAATCTAGTCAAAACTTAAACAGAGGAAGATTAATAAAGACNGGCTGCCTGA
GATAACACTAACACACAC

35

Sequence ID 406
CATCAAATAAATAAATAAATAAATTTTAAAAGTCACAGCATTGAATTTTTAAATGT

TTGGGATGATAAAGCACCTGCTTATCATGAAGCTANAGAAATTCAATGACACGTTT
GCCAGGGTCTTTGCTAGTGATGTTGGAACAAGTCTGTAATGCTGATGAAACATCAC
TGTTCGGGCATTATTGCCCCAGAAAGACACTGACTGCAGCTGATGAAACAGCCCTT
CCAAGAATTAAGGATGCCAAAGACCAAATAACTGTGCTGAGATATACTTACGCAGC
AGGCATGCATAAGTGTAAACTTGCTGTTATAAGCAAAAGCTTGCGTTCTCACTGTT
TTCAAGGAGTGAATTTCATACCAATCCATTATTATGCTAATAAAAAGGCATGGATC
ACCAGGGACATCTTTTCAGATTGGTTTCACAAACATTTTGTACCAGCAGCTTGTGC
TTACTGCAGGGAAGCTGACTGGATGATGACTGCAAGATTTTGTTATATCTTAACAA
CTGTTGTGCTCATCCTCCAGCTGAAATTCTCATCAAAAATAATGTTTATGGCTCAC
ACCTGTAATCTCAACACTTTGGGAGGATTGCCTGACCCAGGAGTTCAAGCCCACCC
TGGGCAACACAGCAAGACCCAACCTNTC

Sequence ID 407
TTTTAAAAATCATAAAACGTTTCTTACAAAGAGCATTACATTNTGCACACTGCTC
TGAACAGATGCCAGGGACATGTGGACTATTGTTACTTTTCCTCCCTGTCCCACCCC
CCAAATGTTACAGTGACCACAAAGCAAGGTGTTCACAATAATTACATGGGGGGAAT
TTTTTAAACCACCAACAATAACGAAAAATAAAATCCACTCACTCTGCTGCTGTTTC
AAAATTTCAATGTTAGTTTTTGCACGCCCTTCCCCCCCCCAACCCTGTTTGTAAGG
AACTAAAACATTACATCTGGTGAACAGCAAAGATTTCACTACACCTCAAATGCAGA
ACACCTATGAAGCAGAGGAATGTTGGCTTTTTAAACAGAAGCAGATAAAAAAAAAA
GATGCAGGACTCCTTCAGTTCTTCACTAGTCTTAGAAAAACTTTCCAGAATACTGC
TTCACACTATAAAAAGAAAAAATATCTTGCATTAGAATCCTTCAACATCTGCATA
CTGCTTCACACTGTTCGTTTCTAGGAGCACTTTGTCACAGGACACTTCTGCTTATA
TTTCTTTAATCAGAACTTAGTTGGATGGGCCGGGCATGGTGGCTCACGCCTGTAAT
CCCAGCACTTTGGGAGGCCGAGG-GGGTGGATCACC

Sequence ID 408
CCATCTCCAAATTTAGTATTCATTCTGTTTAGCATATTATCAGTTGCCATCTATTT
GTTTTAACTGATTACTTGAATCTGATTAAACATCACAGAAATGGGCTTTGATAAGA
ACAATATTGAATAAGAAATTTTAAATAACAAAACAGCTTATAGAAAAATTCAGCAT
AACTTTTCCATCACCTTCACCACCCTTGCCTTTTATTATCCTGTCCTGTATCACTG
CTTTCTGTTAGCAGTGTTGTGTGAGTTAGGATTTGGGCAGGAAAGCAAAGCAACC
ACCCGTCATTTTCCCAGAATGAAGGGTTTGACGTAGGATGTAGACTTTGTATAGTA
GTTGGGAGAGCTGTGGGAGTGAAGGTCAGGGATGTCACCTACAGAAGTCAGGGAAT
CTGCCACCAGAGATCCTGCATCAGAAACAGCCAACAGCGTGCTTCTGAAGAACTAG
TGGGGAAGTGGCTATAATTCTTAGGAATCCCAGCAAGTCCGCACCACTGTCTCAGT
CTACAGCAGTGGAGAAAGGGGTTTCCAGGAGCTCTCTGGAAAGTTCCTGCCCACAC

- 146 -

TTTGCAACAATCTTCAGAGGATAATGGGCTTCTCTTCCAGCTTCCACACCCAACAA
GAGTGCCTTTCATCGGCCAACTCTAACCTGGAACCCTATGGCAGAGGGGATTTAGG
AGACAGTTTGTNATGTCTGTGGAATGCAAATGAANANGTANCAATGCTTANTTGAC
AGCGGNCATACACAAATNTNGAAA

Sequence ID 409
GATCCGTNGACT

Sequence ID 410
CTCTTCCCAGCCCCTGAGCCCAGCCCCTTCCCAAGTGGTGCCAGACAAAAAACTAC
ATGGCCCTTTCGTGTCTTGGGGGTGGAAAGGGAGGGATGAATTGGGGTGATAGAAC
CCTGGTGAATTCAGAGTAATCTTTCTTTAGAAAACTGGTGTTTTCTAAAGAAACAG
GATAGGAGTTTAGAGAAGGCACCAAAGCTTTCACTTTGGTTTGGCACCAGTTTCTA
ACCATCTGTTTTTTCTACCCTAGCTATCTTTTATTGGTAAAATATAAATGTATAAT
TATGTTTGTAGAGCTTTACCAAGGAGTTTCCCTCCTTTTTTGTTTGTTGATTAGCA
AATTTTTGATTCTCCATTTTCCAAAGTAAGAGACTCCAGCATGGCCTTCTGTTTG
CCCCGCAGTAAAGTAACTTCCATATAAATGGTATTTGAAAGTGAGAGTTCATGAC
AACAGACCGTTTTCCATTTCATCTGTATTTTATCTCCGTGACTCCACTTGTGGGTT
T

Sequence ID - 411   nt: 505
TGGAGCTGAAAAATTCCTATTACCTAGGGGCATCACAACGCATTGCATTTCGCCCG
TGTTTGGGATGATGCTGGTGTAAACCTACTATGCTGCCAGTCATGTAAAAGTATAG
CACACACAATTAGTAGGTAATGCTTGCAAATAATAATGAAAGACTCTGCTACTGGT
TTATGTATTTACTATGCTATACTTTTTGTCATTACTTTAGAGTGTACTCCTACTTT
TTTTTTTTTTTTTTTTGAGATGGAGTTTCACTCTTGTCCTGTAGGCTGGAGCGAAN
TGGCGCGATCTCGGCTTACTGCAACCTCCACCTCCTGGGTTCAAGCGATTCTCCTG
CCTCANCTTCCCAGAGTAGCTGAGATTACAGGCATGCACCGCCACGCACGGGTAAT
TTTGTATTTTTGGTAGAGACAGGGTTTCACCATGTTGGCCAGGCTGGTCACCAACT
CCTGACCTCAGGTGACCCGCCTCCTCACCTCCAGAGTGTTGGGATTACAGGNGTGA
G

Sequence ID 412
ATAAAAATTAGCTGGGGGTGATGGGCCCTGTACCCCAGCTACTCGGGAGGTGAGGT
AGGAGAATCACTTGAACCCGGGAGATGGAGGTTGCAGTGAGCCAAGATCGTGCCAC
TGCACTCCAGCCTGTGTGACAGAACAAGACTCTGTCTCAAAAAAAAATAATAATAA
TAATAATAATAAAAGGAATAACATAGCTAGGAATAAATTTAATCAAAGAGGTGAA

- 147 -

AGACTTATACACTTAAAACTACAAAAAAAAAATCACTGAAGGAATTATAGACCCAA
ATAAAAATAAATAAAAAGACATTCTGTGTTTTAGGGAAAGAAGACTTAATATTGTT
AAGATGTCAATACTACCCAAAGTGATCTACAGATTCAACATAATCCCTATCAAAAT
TCCAACAGCCTACTTTGTAGAAATGGAAAGCCAATTTTCAAATTCAGATGGAATT

5   GCGAGGGGTTCTGAATAACAAAACACAATCTTGGGGAAAAAAAACAAAAAACAAAG
TCAAAGAACTCACACTTCTCTATTTATAATTTACTACAAAGTTATAGNATCAAAGT
CGACGCGCCGCGATCCGGGC

Sequence ID 413

10   CACAGTACTCCATTTTGGGGTCCAAACTGTAATGCTCAAAATAATAAATGCTTACA
CGAAAATTATTTATTGAGAATATTCATATAAAAATTACCTAAAGCAAAGTAAAAAA
AGTAAAATCAAGGTGGTATATTTGAAGTGAATGGTGATTGGAAATTTTTAGCTGTA
ACAAAAAGAAAGAAAACAACTTTTTTTAAAGCCTCATTCTCTTTTCTTTCAAAATG
TACCTTATTCCCACACACTCTTGGGCTGACCTTTATTTTATCAATAAGCTCAATAT

15   TACTTTGTTTAAAATAAGATGCTTCAGCAAAGTCATTCTCTCTTTAACCATATAA
TTTAAAAACTCCTCTTCACGATTGATAGCAAAATCAGAAACGTTAGGGCACCAGTG
AGTTGAAAAAACTGGTCTTAAGTTGGAAAAACTATTATTAATAATATTATCCTATC
CATCCATATCTATTGAAATTGTCAGGTCCATAATTTCATTTTAATTAATTATAGGA
AAGAAGAAAGATAATACCCATTTGTTCTAT

20

Sequence ID 414

CTCAGACTCTTTCTGCCCTAATGGCCATTACTATCCAGTCTGTATTGCTACAAGGG
ACCCACTGGTACCCCTTTTAGATTCTATCAAAAGGAACAGGGTTTTCCTAGAGGCA
GGCAGCCTGGTGGTATGGCACAGCAGAAGCTTACTGCTAATGAAATGGGAACCTCC

25   CCCTCCCTTGTGGTTTCAGCACAGAACCTGAATGCCAGGAAAAATTCCTGGGCCAA
GAAGCTAAAGCTAAAGAAACCTTCCTTTTTTCAACGTTTTTTTTTCTTTCAAACTG
TAGGGTCACTTTTGATTGAGGCAAAGGGGTCCTACTGTAAGTGGAAAAGACTCACT
CCCCTAACATAAGTTTTCACTGTGGTGGGATGGTGCCGCCCGATATGCTTGATATG
CTTTTCCTTCCACATGTTAAGCTAGGAAACCTAACAGGATGTCAGCAGGGCAGTTA

30   ACTCTGGACTCANAGCCCTCAAGGGCATGTGGCANAACCTCATGGCATNCAAGACC
A

Sequence ID - 415   nt: 596
GTATAATTGATTCTTTTGAACCTAAAGTATAAGACTTCACGATTAGAAAAAAATTA

35   TCCAAAGACTAATGTAATTAAGTGAGGAAAAGGTGCTGGAGGAACTGGATAACCAC
ATGGAAATGTATGAACCATGACCTCTATGTCACATACTATATATAAAACTTAATTT
GAGGTGTATCACAGAGCTAACTGTGGGGGCTAAAACGTTGAAGCCTTTGGATGGCC

GCACAAGAGATGTCTGCATTCATAACCTTGGGGAGGGTATGAACATTTCTTGGTAA
CATGCAAAAAGCACTAACTGTAAAAGAGAACAGTTGGTCAGTTGAATTTCATGAAA
CATTGTAAACTTCTGCTAAACAACTGACACCATTAAGAATGTGGAAAAAGGCTGGG
CACAGTGGCTCATGCCTATAATCCCAGCATTTTGGGAGGCCGGGGCGGGAGAATCA
5   CTTGAGGCCAGGAGTTTGAAACCAGCCTGGGCAACATGGCAAGACCCCGACTCTAC
AAAAATATTTTTAAAAATTAGTTGGGTGTGGTGATGCACTCCTGTAGTCCTAGCTG
CCAGGANGCTAAGGNGGAAGGATCACTTAACCCTGG

Sequence ID 416
10   CTGGTGGCGGCGGTCGTGCGGACGCAAACATGCAGATCTTTGTGAAGACCCTCACT
GGCAAAACCATCACCCTTGAGGTCGAGCCCAGTGACACCATTGAGAATGTCAAAGC
CAAAATTCAAGACAAGGAGGGTATCCCACCTGACCAGCAGCGTCTGATATTTGCCG
GCAAACAGCTGGAGGATGGCCGCACTCTCTCAGACTACAACATCCAGAAAGAGTCC
ACCCTGCACCTGGTGTTGCGCCTGCGAGGTGGCATTATTGAGCCTTCTCTCCGCCA
15   GCTTGCCCAGAAATACAACTGCGACAAGATGATCTGCCGCAAGTGCTATGCTCGCC
TTCACCCTCGTGCTGTCAACTGCCGCAAGAAGAAGTGTGGTCACACCAACAACCTG
CGTCCCAAGAAGAAGGTCAAATAAGGTTGTTCTTTCCTTGAAGGGCAGCCTCCTGC
CCAGGCCCCGTGGCCCTGGAGCCTCAATAAAGTGTCCCTTTCATTGACTGGAGCAG

20   Sequence ID 417
GCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCCGCAGATAAGTTT
TTTTCTCTTTGAAAGATAGAGATTAATACAACTACTTAAAAAATATAGTCAATAGG
TTACTAAGATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATT
TTAAGAGAAAATATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGG
25   TTTCTAAAACATGACGGAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTAT
TTAAAAGAAAATTGAGAGAAAGGACTACAGAGCCCCGAATTAATACCAATAGAAGG
GCAATGCTTTTAGATTAAAATGAAGGTGACTTAAACAGCTTAAAGTTTAGTTTAAA
AGTTGTAGGTGATTAAAATAATTTGAAGGCGATCTTTTAAAAAGAGATTAAACCGA
AGGTGATTAAAAGACCTTGAAATCCATGACGCAGGGAGAATTGCGTCATTTAAAGC
30   CTAGTTAACGCATTTACTAAACGCAGACCAAAATGGAAAGATTAATTGGGAGTGGT
AGGA

Sequence ID 418
CCCGGAATCGCGGCCGCGTCGACGGGAGGTGATAGCATTGCTTTCGTGTAAATTAT
35   GTAATGCAAAATTTTTTAATCTTCGCCTTAATACTTTTTTATTTTGTTTTATTTT
GAATGATGAGCCTTCGTGCCCCCCCTTCCCCCTTTTTTGTCCCCCAACTTGAGATG
TATGAAGGCTTTTGGTCTCCCTGGGAGTGGGTGGAGGCAGCCAGGGCTTACCTGTA

- 149 -

CACTGACTTGAGACCAGTTGAATAAAAGTGCACACCTTATAAAAAA

Sequence ID 419
CCCGGAATCGCGGCCGCGTCGACGGGAGGTGATAGCATTGCTTTCGTGTAAATTAT
GTAATGCAAAATTTTTTTAATCTTCGCCTTAATACTTTTTTATTTTGTTTTATTTT
GAATGATGAGCCTTCGTGCCCCCCCTTCCCCCTTTTTTGTCCCCCAACTTGAGATG
TATGAAGGCTTTTGGTCTCCCTGGGAGTGGGTGGAGGCAGCCAGGGCTTACCTGTA
CACTGACTTGAGACCAGTTGAATAAAAGTGCACACCTTATAAAA

Sequence ID 420
CTTCATTTGAAATGGTTGAATCTGCTGTGTAATAAAGTGGTTCAACCATGATTAGG
AACTGAAATTTAGTAGAAGAGGGAAAAGGAGTTAATGTAACAAATTATTTTAGCTA
CAAACCCCGGTAATAGAGCACTTGGGGGATGGGATGGGGTGGGTTGGTGAGACAAT
CAGAATGGTAAATTGATTAAATGCTCCTAACCCTGTAATTTTGTGCATAGAGCACC
CTATGCTGTGGAAATAACTGTTCTTAGATTTCATTGTAACTGGACTGTTCAGGTTG
CCCAGAGGGAAAGAACATTCCTAATTCTAATAAAATAAACTTTTATTTTGTTTA

Sequence ID 421
TGTCATTGAATCTGCTTGTTACTTAAATGCTAAACTCAATTCTGTAATTCAATAGG
TGCACCTCTCTGAGAAACATAAGAGACAATGAGGAAAAGGATTCAGCATTCCGTGG
AATTTGTACCATGATCAGTGTGAATCCCAGTGGCGTAATCCAAGTAAGATGTTCAC
AAAGATTTGTTTTTAATGTCTAATTAATAAAATTTTAAAGGAAGAAACATTCTAAT
ACTTTAATTATAAAAAGTTAACTATTTTCAAAGGTATCAAAATACAGTTAAACCTT
TAAAATGTATATTTCTTAATATCTTGAAATTGTAATGCCTTTTTTTTTTCCTAAAT
TTTTTTGTCATGAAATGAGATAGTAACAGCAGATTGGGACAACAAGGTTATATTC
TTGTCTTGAATCAGGCCATGGCTTCTTTCATCCAAATTTCAGACCTCATTTATTTA
CTTTGTCCCTGCCTCCCATCCCTGGATATCAGTTTGTGGATATCTACAGTTAATAG
AGTGACCAAATAGTAGGAATACTGTCTCTCTATTCTGAATAAAATCTTTGAATCAG
ATTTAGAAATAATGAATAAAATACAAATCAGCCATTGAAATTGCTCTAATTTTGAG
AGCTTATGATTTATTCATCTTTGGTTTCCAAGTTCAAGTTATATGTAGACATTTTA
ATT

Sequence ID 422
GCTTCCTAGGTGAGGTCACGAGGAAACCTGCTGGCCAAGTGACCTGGCAGGGTGTG
GCCAGTGTGGCCAGGGCCGCCGAGCCTGCTTTCCTTCCCTGCAGCAGGAACCCTTC
TGGGGCTGTGATCCTGCGATGGTGCCTGGGTGGGAGTGGGGGTGGGGGGCGGGATG
GTCTCCCTACCTGCCAGCTTCTTGGTTTGAGGTGAGGACAGCCCCGGAAGCTCANA

- 150 -

CTTGGCTCCTGTCCATGTACTTGGGGCCATGAGCTCTGCAGGGACCTTGGAAAGAN
AGAGACGGGTGGTGTANGGCANGGGAAGGCATTGTCTTCAAACAGGAAAAAGCTGA
NAATGGAAACAGGCGAAACTTACCAAGTGTAACATCACCTGGAACTGAAGGAGGGT
GGGAAGGTTTTAATTATTTTAAAAATAGAGATGGGGTCTCACTATGTTGCCCAGGC
TGGTCTCAAACTACTGGGCTCAAGTGAACCTCCTTCT

Sequence ID - 423   nt: 387
TGTTTCTCNAGGGCGAGAGGCTGTCTTANAGCACCATTCTCTGGCCCTNGTCCCAT
GAGAAGGAACCGCACTCAGGAGCCACACTCTCCCACTNCCCTTGCCCANAAGACTC
ACAGAGGGCACGGAGCTGGCTGTGGTGAGAGGAGGTCCANCAAATTCCTGTCTGCA
NAAGGGTTCTGAACACCACCGCCTGGCAGCGTGCTGGAGGAGGGATTCCTCTTTTC
CTCACAGCAATTCTGACCAGAAACCTGTCAAATCAGGAATGGCTAAAATAAGACCA
GGGTATGAATGACCATCAGCCACAGTAAAACCAAGGCACAGCTCTCCTGAGCCCAC
CCAAGCTGCTGTGGCCCAGACTGGTGACATCACCTCAGGGCAAAAAAAAA

Sequence ID - 424   nt: 420
CGCAGAATGGCTCCCGCAAAGAAGGGTGGCGAGAAGAAAAAGGGCCGTTCTGCCAT
CAACGAAGTGGTAACCCGAGAATACACCATCAACATTCACAAGCGCATCCATGGAG
TGGGCTTCAAGAAGCGTGCACCTCGGGCACTCAAAGAGATTCGGAAATTTGCCATG
AAGGAGATGGGAACTCCAGATGTGCGCATTGACACCAGGCTCAACAAAGCTGTCTG
GGCCAAAGGAATAAGGAATGTGCCATACCGAATCCGTGTGCGGCTGTCCAGAAAAC
GTAATGAGGATGAAGATTCACCAAATAAGCTATATACTTTGGTTACCTATGTACCT
GTTACCACTTTCAAAAATCTACAGACAGTCAATGTGGATGAGAACTAATCGCTGAT
CGTCAGATCAAATAAAGTTATAAAATTG

Sequence ID 425
GGAAACTGATGCCAGTCAGAAACTCAGATCAAATGAAGGGGTGAAGAGAACCAGAA
TTGATCTCTCTGTAGGAGAATATAAATGACTTTTTTAAAGTACATATTTTCTGTGA
AAGACAGTTTTTTGTTTAATGCAAAAATGTTAACAATGTTTATATCATGTAGAAGT
AAAAGATCGTGAAACAGCACAGAGAACAGTAGTAAGACAGATTGAATTGCACTGTT
GTAAGATGATGAACTTACAATATTAAGTGAAGGTAGACTGTGATAGATTAAGGATA
TATATTGTAATCCCTAGAGCAATTGTCAAAGTGGTACAGGTAAAAAGCCAATAGAG
GTGATAAAATGGAATACTAAAAAATATCAGATGAATAATAAAGAAGACAGGAAATG
AGGAACAGTGGAACAGAATGAATAAAAAACAAGACCATTAACTTAATCATTAATAA
TTACTTTAAATGGGTTAAACATTATGGTTATAAGGCAGAGATTTTCAGACTAGATA
AAAGAGCAAGCTCCACTATATACTGTCTACAAGAGATATACTTTAAAGTGTATATT
ATATTTAAATATAAAGATTTGGAATAAATAAACCTAAGAATAAGCTTACTAGGGAA

GTGAAAGATCTGTACAACAAGAATTACAAAACACTGCTGAACGAAATCATAGGTGA
CCA

Sequence ID 426

GTCCCGGAATCGCGGCCGCGTCGACGTTTCCTCAAAATTTATCTTCCTGTTAATGT
CAGGCATGTATCTCCTTAGCTTGCCACAAATAACTATATATACCACAGACCTTCCT
TTGTAGGGCTAACAGTGTTGCATTGTAAGTGGAGGCCTCATAGATACCTGGCCTTT
TCCTACCTTATTCCAAAGATGGTTGCATCTTATAAATAATGTCATTCTTCAGCAAA
TGGTATGGAAATGAGATTGTAATGTCATTATTTCCTCTTTAAATAATCAGGACAAC
TCATGATACAAAGAGCTCTTCTCTATAAAAGGTGGGACTTTTTTTTTAGTAATAG
CAAAAATAAAATTGTACCTCCTTAATCTTCTACAGAAAGATGGATTTCATTTTCAA
CATTAAGAGGTAGTTTTAAGAAGCAGTAGAAGTCAGCCTGGGCAGCATGGTGAAAC
CCCGTCTCTACAAAAAGTTAGCTGGGCTTAGTAGTTGCAATCCCAGCTACTCTGG
AGGCTGAGGTTGGAGATCATCTGANCCTGGGGAGGTCNAGGCTGCAATGATACANT
GAGCCCTGATTGTGCCACTCCACCTGGTTGCAGA

Sequence ID 427

TTCCAATCTTCGTGTTCACTTTAAGAACACTCGTGAAACTGCTCAGGCCATCAAGG
GTATGCATATACGAAAAGCCACGAAGTATCTGAAAGATGTCACTTTACAGAAACAG
TGTGTACCATTCCGACGTTACAATGGTGGAGTTGGCAGGTGTGCGCAGGCCAAGCA
ATGGGGCTGGACACAAGGTCGGTGGCCCAAAAAGAGTGCTGAATTTTTGCTGCACA
TGCTTAAAAACGCAGAGAGTAATGCTGAACTTAAGGGTTTAGATGTAGATTCTCTG
GTCATTGAGCATATCCAAGTGAACAAAGCACCTAAGATGCGCCGCCGGACCTACAG
AGCTCATGGTCGGATTAACCCATACATGAGCTCTCCCTGCCACATTGAGATGATCC
TTACGGAAAAGGAACAGATTGTTCCTAAACCAGAAGAGGAGGTTGCCCAGAAGAAA
AAGATATCCCAGAAGAAACTGAAGAAACAAAAACTTATGGCACGGGAGTAAATTCA
GCATTAAAATAAATGTAATTAAAAGG

Sequence ID 428

TGCAGGATCCGTCGACTCTAGATAACATGGCTAGAAAAGAGAATGAAAAAGTTGGA
ATTTTTAATTGCCATGGTATGGGGGGTAATCAGGTTTTCTCTTATACTGCCAACAA
AGAAATTAGAACAGATGACCTTTGCTTGGATGTTTCCAAACTTAATGGCCCAGTTA
CAATGCTCAAATGCCACCACCTAAAAGGCAACCAACTCTGGGAGTATGACCCAGTG
AAATTAACCCTGCAGCATGTGAACAGTAATCAGTGCCTGGATAAAGCCACAGAAGA
GGATAGCCAGGTGCCCAGCATTAGAGACTGCAATGGAAGTCGGTCCCAGCAGTGGC
TTCTTCGAAACGTCACCCTGCCAGAAATATTCTGAGACCAAATTT

Sequence ID - 429   nt: 535
CACAGTACTCCATTTTGGGGTCCAAACTGTAATGCTCAAAATAATAAATGCTTACA
CGAAAATTATTTATTGAGAATATTCATATAAAAATTACCTAAAGCAAAGTAAAAAA
AGTAAAATCAAGGTGGTATATTTGAAGTGAATGGTGATTGGAAATTTTTAGCTGTA
ACAAAAAGAAAGAAAACAACTTTTTTTAAAGCCTCATTCTCTTTTCTTTCAAAATG
TACCTTATTCCCACACACTCTTGGGCTGACCTTTATTTTATCAATAAGCTCAATAT
TACTTTGTTTAAAATAAGATGCTTCAGCAAAAGTCATTCTCTCTTTAACCATATAA
TTTAAAAACTCCTCTTCACGATTGATAGCAAAATCAGAAACGTTAGGGCACCAGTG
AGTTGAAAAAACTGGTCTTAAGTTGGAAAAACTATTATTAATAATATTATCCTATC
CATCCATATCTATTGAAATTGTCAGGTCCATAATTTCATTTTAATTAATTATAGGA
AAGAAGAAAGATAATACCCATTTGTTCTAT

Sequence ID 430
CAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGTTTTT
TTCTCTTTGAAAGATAGAGATTAATACAACTACTTAAAAAATATAGTCAATAGGTT
ACTAAGATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTT
AAGAGAAAATATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTT
TCTAAAACATGACGGAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTT
AAAAGAAAATTGAGAGAAAGGACTACAGAGCCCCGAATTAATACCAATAGAAGGGC
AATGCTTTTAGATTAAAATGAAGGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAG
TTGTAGGTGATTAAAATAATTTGAAGGCGATCTTTTAAAAAGAGATTAAACCGAAG
GTGATTAAAAGACCTTGAAATCCATGACGCAGGGAGAATTGCGTCATTTAAAGCCT
AGTTAACGCATTTACTAAACGCAGACGAAAATGGAAAGATTAATTGGGAGTGGTAG
GATGAAACAATTTGGAGAAGATAGAAGTTTGAAGTGGAAAACTGGAAGACAGAAGT
ACC

Sequence ID 431
CGCTGGGTGCCTGCAGCGCCTCCCTTGTCTCATATGGTGTGTCCAGCACTCTATTG
TTGTAAACTGTTGNTTTGNCTGACCTAAATTNTCTTTACTAAACANATTTAATAGT
TNAAAAAAAAAAAANANCA

Sequence ID 432
TTTTAAAGTCATCTCTATAGGAAGGTGCTGGGCAGGGATCCCAGAGAAAGAAAGGG
TCCAAGACTCCATTAACTGCCCTGGATGAAGGGCACTGCTACAGCAGCTAGTACCA
GAGACTCTCCTATCTCACGGTTGAGGCAGACCCAGGATAGAATAGAGAATAAAAGG
AATGCTTATAGGAAACAATTTTGTATGGAATGCTAGATGGCCAAGCCTCAGCCTTT
GGTCCAGTGCAACCCTTGCCTCGCTTGTCAACAGTGAAAAATTAGTTTGGTTAGAA

- 153 -

GAACCATCTGGAAACACACCAGCTTCTGCTACCTTCATGCTCATTGTTAAAAAAAG
ATTAACCAGTGTGAACATTCTGATCTGTTAATTCCAGGGACTGTTTTCTTTCCAAT
GGACTGTTTGTTGGTAGAATAACCCCCAAAAGCTCAAAGCTAAAATGCATCATCAG
TCCTAGTCGGCAGTTCCTTAAGAATGGACTGGCGGCGTGGTTGAGCTGATATGGAA
AAGCTGCACCTTCCTGCAGAAGATCAACTGACCTGCTATCCCACCCCAAATTTCAA
CCTGAGGTATATTTCAATGAAGGCAGGTAGCTGTGCTTCTCAGAGCA

Sequence ID 433
TCCCGGAATCGCGGCCGCGTCGACCCGCCGCCGAGGATTCAGCAGCCTCCCCCTTG
AGCCCCCTCGCTTCCCGACGTTCCGTTCCCCCCTGCCCGCCTTCTCCCGCCACCGC
CGCCGCCGCCTTCCGCAGGCCGTTTCCACCGAGGAAAAGGAATCGTATCGTATGTC
CGCTATCCAGAACCTCCACTCTTTCGACCCCTTTGCTGATGCAAGTAAGGGTGATG
ACCTGCTTCCTGCTGGCACTGAGGATTATATCCATATAAGAATTCAACAGAGAAAC
GGCAGGAAGACCCTTACTACTGTCCAAGGGATCGCTGATGATTACGATAAAAAGAA
ACTAGTGAAGGCGTTTAAGAAAAGTTTGCCTGCAATGGTACTGTAATTGAGCATC
CGGAATATGGAGAAGTAATTCAGCTACAGGGTGACCAACGCAAGAACATATGCCAG
TTCCTCGTAGAGATTGGACTGGCTAAGGACGATCAGCTGAAGGTTCATGGGTTTTA
AGTGCTTGTGGCTCACTGAAGCTTAAGTGAGGATTTCCTTGCAATGAGTAGAATTT
CCCTTCCTCCCTTGTCACAGGTTTAAAAACCTCACAGCTTGTATAATGTAACCATT
TGGGGTCCGCTTTTAACTTGGACTAGTGTAACTNCTTCATGCAATAAACTGAAAAG
ACCATGCTGCTANTC

Sequence ID 434
TTCGGACGCAAGAAGACAGCGACAGCTGTGGCGCACTGCAAACGCGGCAATGGTCT
CATCAAGGTGAACGGGCGGCCCCTGGAGATGATTGAGCCGCGCACGCTACAGTACA
AGCTGCTGGAGCCAGTTCTGCTTCTCGGCAAGGAGCGATTTGCTGGTGTAGACATC
CGTGTCCGTGTAAAGGGTGGTGGTCACGTGGCCCANATTTATGCTATCCGTCAGTC
CATCTCCAAAGCCCTGGTGGCCTATTACCANAAATATGTGGATGAGGCTTCCAAGA
AGGAGATCAAAGACATCCTCATCCAGTATGACCGGACCCTGCTGGTAGCTGACCCT
CGTCGCTGCGAGTCCAAAAAGTTTGGAGGCCCTGGTGCCCGCGCTCGCTACCAGAA
ATCCTACCGATAAGCCCATCGTGACTCAAAACTCACTTGTATAATAAACAGTTTTT
GAGGGATTTTAAAA

Sequence ID 435
CTGCAATGTGCAATAGTTGCACCACTGCACTCCAGCCTGGGTGACAGAGTGAGAAC
CTATCTCTTAAAAAAAAAAAAAAAAAAAAGGAAGAAGAGACATGAGAGGGCCCAAGT
CACTTGCTCACTCACTTTCCGTGTACATGTACCAAGAAAAGGCCATGTGGGAAAGA

GCAAGAAGGCAGCCGCCTTCAAGACAGGAAGAGAGCCCTCACCAGAAACTGAGCCA
GAACCTTGGAATTCCAGCCTCCANAACTGTGAGAAAAGAATTTTCTGTTGTTTCAG
TCCCCCACACTATGGCATTTTGTTACGGCAGCCTGAGCTAATACTCCTACTTTGTC
CTGCATTTACTTGGTCTTCCAGTTAGTTTTTTAGACTTTGGGAATCAGAGCAGTCA
5   GTTGTCAGATTTTAGCTTACAGTTGTCCTACCTGTGCAACTGAAATTTCTTCCATT
TTAAACCAGAGCAGAGTTTTAGAGTCAAAAGAAACCAGATCTTTTAGTGCAGAAGC
TTTCCACTGTATTANAAGTGAGGAAGTTGGT

        Sequence ID 436
10   AAAAAAACTCCAGAGAAGTTTATAGAAAGAGATGACATGTAAACCCTGCTGAAAAA
TAGTTTCATTTGTTAGAATATAATTGTCTTCCACTAAAAAAAGAAAAAAAAAAGCA
TTTAAGGCTCTAAGATCTCTTGAAGTACCACTTTTCCTGAATCCCAGAGTTTTTAT
GTGCATTATTTTTATGCGTTTGTAGTTTGATATGTTGTATTTATAAGTAGTTTTAG
CTTTCCATTATGAATTCTTCTTTGACCCATGAGTTATTTAGGTAAGTGTTTAAAAA
15   TTACAATAGTTTATATATGCAAATATTATGTTGTTAGAGTTGGTTTTCATGTCAT
TTTTACATATACAGGGGCAGTTTCCCCAACTAAATTGTATATTCCTTAAAGCAGCA
CTCTTAAATTTTATTTCTGTGTCAATTTCTTGNCTGTGTTTCCTGGCATGGAATAC
ATGGCATAAAATTTGTTATGTAATTAAATGAAATATTATTATACTTTCTATTTTTT
AGAAAAAA
20

        Sequence ID - 438   nt: 577
GTCGACAGGGATGACATAACTATTAGTGGCAGGTTAGTTGTTGGTCACTTTCAACT
CTGGGTTCAAGCGATTCTCCTACCTCAGCCTCCCGAGTAGCTGGGATTACAGGCAT
25   GCACCGCCACACCTAATTTTCTATTCTTAGTAGAGACGGGGTTTCTCCCTGTTGGT
CAGGCTGGTCTCGAACTCCCGACCTCAGGTGATCTGCCTGCCTCAGTCTCCCAAAG
TCCTGGAACCACAGACATGAGCCACCACGCCTGGCCCCTTTTAAAATATTTCTGCT
CATTGATGATGCACCCAGTCACCCAGTGCTCTGATGGAGATGTATAAGGAGATGA
ATGCTGTTTTCATGGCTGCTAATACAACATTCATTCTGCAACCCCCAAATCAAGAA
30   GTAATTTTGACTTTCAAGTCTTATTATTTAAGAAATATATTTTGCAAGACTATAGC
TGCCATAGACCGTGATTCCTCTGATGGATCAGACAAACTAAAATGAAAACCTCCTG
CAACGTATTCATCATTCTAGATCCCTGAGGAATCGCCACACTGACTTNCACAATGG
GTGAACTGGGTTACAGT

35   Sequence ID - 441   nt: 552
AAACAAAATTATTCTCTGAGAGGGAAAGGACATTTGAGGGAAACATCAAATTTCCC
CATAAATAAATGAATGGAGTTTGCAGGAAGGTGAGGGTGAGCAGAGATGTGTGTGG

- 155 -

ACATCTCTGACCATCCATCGCTGTATTCAAATGGATTGTTTTATTCCATTCTGGTC
TCAGGCATGACCACGTCCAGTGAAGACATTTGAGGCAGCACATCTCAGGACCCAGG
CAATAGACTGGCCCCAACTCAGGCTGGACTAAGGTGTGATTAATTCTTTGTTTTTT
GTGTGGAACAGCTCACCTTGTCAGACAGCCTCAGGGCATCTCTGAGACACAGGGGC
AGAAAATGACATTCATCTTTTGAGTCCTCATCCATGGAGTGCTGTGTTTGGGGGGC
TGCATCTGCTGAAGCGAGAACCCCATTCTGCCACCCCACCAGGATGCCCATTCTCC
AGGACTTCTCCAACTTACTATTAGACTAAACCAGAACAAGCAACAAACTGTATTTA
TGCAAGCAAAATTGATGAGAAATTATATTCAAATAAAGCAAAAATTA

Sequence ID - 442   nt: 606
TCGTGCCACTGCACTCCAGCCTGGACGACAGAGTGAGACTCCATCTCAAAATAAAT
AAATAAATAAATAAATAAATAAATAAAAAAATAAAAAATACTTCTGCTATGA
AAAACCTAGTTGGTATTTTTGCTTATTTAATACTATAGAAATATGGTGATCTCATC
TTTAATAGAGTGCTTTTAAGGTCCCCAGTGATAATCTCCTAAAATCATGAACTTTA
AGAATTTATAATGTTAATATGAGGAAATGAAATCTGGATTATCTCACCACATATTA
TATAATTCATTAGTGACAGAGCAAGAACTCCAGGTCACCTGTCTATTCCATGTTTT
TCCTATCTGCCTTTAAATGTTGAGATACTACCCTTATCTCATGTGAATGGAGAAAC
TGCCTAAAATGCTAAAACTGACTCAGAGGCACCCAGACATAAGTGAAGTGTGATTA
GAAAATCCTGGTCAGTTGAGTCTTAGCCAAATGTGTACCTACTGTGTCTGCCTCTA
TCAAGTCAATGAAAACATGATCTGAGAACTGTAAGTCCATTTATGGAAAGGGTTGA
TTTANAGATATTTTGAACTTNCAGTGATGAGCCCCTTCTCAAATAG

Sequence ID 446
CGGACTCCTGTGCTAATTGTCAGCTTACATATCATTGTATAGAGACTGTTTATTCT
GTACCAAACTGATTTCAAAAGTACTACATNGAAAATAAACCGGTGACTGTTTTTCT
TCATAAAGTTCTGCGTTTGGCATCTTCACTCTTTCCAAAATGTATCTGTACATCAN
AAATGTCACTATTCCAAGTGTCTTTTTAGTGTGGCTTTAGTATGGCTTCCTTTTAA
TATTGNACATACATTGNATCTTTGTTTTATGGNAATAAGTAATAAAAATGTAGACT
TCATATTTTGTACAAAATGTCCTATGTACAGAATAAAAAAGTTCATAGAAACAGCC
NANAA

Sequence ID 447
AGGCCGAGGCAGGCAGATCNCNTGAGGTCAAGAGTTTGAGACCAGCNTAGCTAACA
TGGTGAAACCCCATCTCTACAAAAATATA-AAAATTAGCCTGG-GTGGTGATGGGC
ACCTGTAACCCCAGCTACTCGGGAGGCTGAGGTAGGAGAATCACTTGAACCCGGGA
GATGGAGGTTGCAGTGAGCCAAGATCGTGCCACTGCACTCCAGCCTGTGTGACAGA
ACAAGACTCTGTCTCAAAAAAAAATAATAATAATAATAATAAAAAGGAATAAC

ATAGCTAGGAATAAATTTAATCAAAGAGGTGAAAGACTTATACACTTAAAACTACA
AAAAAAAATCACTGAAGGAATTATAGACCCAAATAAAAATAAATAAAAAGACATT
CTGTGTTTTAGGGAAAGAAGACTTAATATTGTTAAGATGTCAATACTACCCAAAGT
GATCTACAGATTCAACATAATCCCTATCAAAATTCCAACAGCCTACTTTGTAGAAA
5   TGGAAAAGCCAATTTTCAAATTCAGATGGAATTGCGAGGGGTTNTGAATAACAAAA
CACNATCTTGGGGAAAAAAACAAAAAACAAAGTCAAAGAACTCACACTTCTNTAT
TTATAAATTTACTACAAAGTTATAGTAATCNAA

Sequence ID - 448   nt: 329
10   TACGCACACGAGAACATGCCTCTCGCAAAGGATCTCCTTCATCCCTCTCCAGAAGA
GGAGAAGAGGAAACACAAGAAGAAACGCCTGGTGCAGAGCCCCAATTCCTACTTCA
TGGATGTGAAATGCCCAGGATGCTATAAAATCACCACGGTCTTTAGCCATGCACAA
ACGGTAGTTTTGTGTGTTGGCTGCTCCACTGTCCTCTGCCAGCCTACAGGAGGAAA
AGCAAGGCTTACAGAAGGATGTTCCTTCAGGAGGAAGCAGCACTAAAAGCACTCTG
15   AGTCAAGATGAGTGGGAAACCATCTCAATAAACACATTTTGGGTTAAAA

Sequence ID 450
GAGCAGTGGCATGATCACACCTTACTGCGGCCTCCAACCCCTGAGCTTAAGTGATT
CTCCCGCATTATCCTCCTGAGTAGCTGAGACTACAGGTGCATGCCACCATACACTA
20   CTAAATTTGGGTCGGGTGGTGGTGGTGATTTTTTAATATTTTTGTAGAGACAGGGT
CTCACTGTGATGCCCAGGCTGGTCTTGAACTCCTGGGCTCAAGCAGTCACCCACCT
CAGCCTCCCAAAGCACTGGGATTACAGGTGTGAGCCACCACACTGGCCAGCTTTGT
TTTGTTTTGATGACTAAGCTGCTCTTGCTAAAAGGGCTTCTCTCTGAACTTCCCTA
CCTTTCTTCTGTTTCCCTGGGCTAGGGCTCCATGTTGGCAGTCCTACTCCCAATTA
25   ACCTGGGGCTGTCTGGTTAACCTTTATAAGATCTGCAGTCATTGGGAGACCCGGGG
ACCAGGAATATTGTTGTTGAGGGAGCTACCCTGGAAAGTGGATGGGTGGCCAAAGG

Sequence ID 452
TTTGGCTTTGCCTCTAGGCATTAGATGTTATCTTTGGAGGCATCCTTCTATGAGCA
30 .   TTCATTTTTGGACCAAGCCTGGATTTACAATTCTATTACTGGCCCAGACTTCATTT
CTATCCAATTTCATTCCACTGTGCTATAGTTTACAACATATAATTTGACTTATAAA
TAATTCCTGACTATGGGTTTAAAGACTGAAATGGATCAATAGAAACTTTGAAAAT
GTTAACATCTTGATTGCTTTTCTCAGTGTAGAAATGGACAATGTTTAGCTTAAAAA
CTGCATGTTTTTAATGAGATACGGGGTTGAAAGACTTATTCCTGGAATTTATTGTT
35   CTGGAGAAGCCTGTTGCTATCTGCCATACCTTGGTTTACTTTGTGCAAAATGAGC
TTCTTTTTAAGTAATGAGCTCTTTCCATGTTCAGCTTAAATTGCTGTCTTAGACAC
TTCATCAGGGTTCCCTGCTCTGCCTCATTCCCCCTTTTGCTCACTTGCAGCCTTTG

ACATAATCCTGGGAGGCAATTGGCATCATACATATTTTGCTTTGTAATCTCCTGCT
TTGATTCTGACTGGGACCCAGC

Sequence ID - 453   nt: 747

GGATCTAAGACCAGCCTGGCAGCCACCAGATGGTGATTCTAGTCCTGGCTCAGTCA
GTAATAGGTCACTGACCCCAGAGAAATCAATTCAGCCTCCCCAGGTCCTTGGATTT
CTTTCTGTGAAAATGAAAGCATAGGTAGGAATTTCCCATGGAACAGCTAGCAGAGG
AGAAATATTAAAAGTCAGGAGACTCATGCTATAGTTTTCATACTTCATTACAACAA
TGTTGTTTAGGACAAGTGAGTTAACCTGTTAGCTTCCTCTATATAAAATGGAAAGT
CATTAAAAACCTACATAGCAGGGTTCTTGTGAAGATCAAGTGATAATGTAGGAAGC
ATGTACAAATGTCACATTCTGCCGTCACGTAATGGTCCTCACAGCTTGAGGTAGCA
TTTAGCATGTGTCATGATTTAGTACAAGGGTTGGCAAACTGTTGCTCTTGGATTAA
GTCTGGCTCATTGCCTGTTTTTCAAAGAAAAAAATTGTATATGTGTGTATATATGT
TATATATAGGTACACACACATATGTGCTATATATAGCATATATACACACATAATAT
ATAAACATGTACATATATAGCATTATATATATACCGTGTATAATATCTCCAGTCCT
CATGACCAGCCATGCTTGTTCATTTACATTTGCATACTCTATGATTGCTTTCATGC
AACAATGGCAGAGTTGAGTGATTGTTTTGCACAGANACTGTATGGCCCACTAAACC
TAAAATATTAATCTCTGCC

Sequence ID 454
CTCCTGCCGGGCTCGTGGCGGCTTCTGTCCGCTCCGCGGAGGGAAGCGCCTTCCCC
ACAGGACATCAATGCAAGCTTGAATAAGAAAAACAAATTCTTCCTCCTAAGCCATG
GCATATCAGTTATACAGAAATACTACTTTGGGAAACAGTCTTCAGGAGAGCCTAGA
TGAGCTCATACAGTCTCAACAGATCACCCCCCAACTTGCCCTTCAAGTTCTACTTC
AGTTTGATAAGGCTATAAATGCAGCACTGGCTCAGAGGGTCAGGAACAGAGTCAAT
TTCAGGGGCTCTCTAAATACGTACAGATTCTGCGATAATGTGTGGACTTTTGTACT
GAATGATGTTGAATTCAGAGAGGTGACAGAACTTATTAAAGTGGATAAAGTGAAAA
TTGTAGCCTGTGATGGTAAAAATACTGGCTCCAATACTACAGAATGAATAGAAAAA
ATATGACTTTTTTACACCATCTTCTGTTATTCATTGCTTTTGAAGAGAAGCATAGA
AGAGACTTTTTATTTATT

Sequence ID - 458   nt: 682
TGCCACTGAAGATCCTGGTGTCGCCATGGGCCGCCGCCCCGCCCGTTGTTACCGGT
ATTGTAAGAACAAGCCGTACCCAAAGTCTCGCTTCTGCCGAGGTGTCCCTGATGCC
AAGATTCGCATTTTTGACCTGGGGCGGAAAAAGGCAAAAGTGGATGAGTTTCCGCT
TTGTGGCCACATGGTGTCAGATGAATATGAGCAGCTGTCCTCTGAAGCCCTGGAGG
CTGCCCGAATTTGTGCCAATAAGTACATGGTAAAAAGTTGTGGCAAAGATGGCTTC

- 158 -

CATATCCGGGTGCGGCTCCACCCCTTCCACGTCATCCGCATCAACAAGATGTTGTC
CTGTGCTGGGGCTGACAGGCTCCAAACAGGCATGCGAGGTGCCTTTGGAAAGCCCC
AGGGCACTGTGGCCAGGGTTCACATTGGCCAAGTTATCATGTCCATCCGCACCAAG
CTGCAGAACAAGGAGCATGTGATTGAGGCCCTGCGCAGGGCCAAGTTCAAGTTTCT
5   GGCCGCAGAAGATCCACATCTCAAAGAAGTGGGGCTTCACCAAGTTCAATGCTGAT
GAATTTGAAGACATGGTGGCTGAAAAGCGGCTCATCCCANATGGCTGTGGGGTCAA
GTACATCCCCAATCGTGGCCCTCTGGACAAGTGGCGGCCCTGCACTCATGAAGGCT
TTCAATGTGC

10   Sequence ID 459
TCCCGGAATCGCGGCCGCGTCGACCTTGTCCTTGAGCGTCAACCTTCTTTCCCTGA
AGTGGCTGGGGTTCCTGTTTCCTTCTTTGATTGACAACTTGTGTTAACCCTCGCAC
ATCTCTGGGCCAATTTTTGCTTGTAAGTCTTTCCGGAGACCCCTGGAATTTAAATC
ATTAGCACCGCGCCCTTCCCCGAAGAGTCTTCGAAGGGTTGCCGCTTTTCGGTGGC
15   GCAGTTCTCGCGAGAAGGTGACTTTCTTTCTCGGTATTTCCTGGTTTCCAGAATCC
TTAGCGCGAGGCGGAAAAAATATTTCTCCCAGCTTGTGTTGATGCCGCGATTTTGA
CTGAGACTTCTTCCCACGATTTCTGTTTTTGCTTCTCCAAGGAAAATGGCAGCTCC
CGAGCAGCCGCTTGCGATATCAAGGGGATGCACGAGCTCCTCCTCGCTTTCCCCGC
CTCGGGGCGACCGAACCCTTCTGGTCAGGCACCTGCCGGCTGAGCTTACTGCTGAG
20   GAGAAGAGGACTTGCTGAAGTACTTCGGGGCTCAGTCTGTGCGGGTCCTGTCAGA
TAAGGGGCGACTGAAACATACAGCTTTTGCCACATTCCCTAATGAAAAGCAGCTN
TAAAGGCATTGACAAACTNCATCAACTGAAACTTTTAGTCATACTTTAATCG

Sequence ID - 460   nt: 536
25   CAGAGATCAAAATAGGCCTTACACAGTGCGACGCGAATTTAAAAGATTACCCCATT
CAGGTGTATGGATTTTGCAGTATTAAAGATGCTGCCTGGAATAGGTCATTATCTTC
TCCAAGTACTCTGTTAAGTCAATGAGTCACATAGAGTATAAGGTTTATTATCTGCT
TTTCTTTCATTAAATAAATCTTTATTGAATTTCTACTACATTAAAAAACCAAACCA
AAACAAAACAAACAAAAAAACACTTCCCTGAGCCATAAAGGAGAAGGTAGTTTTG
30   ACTGGAACCTTGAAGGATGGGTAAACTTTCAGCAGATAAAGATTGAGAGAAGACCT
TCCAGGTAGAGAAAGCAGTGTGGGCACAGGCAAAGATGGAAGAACACACGTGGCTG
TGGGAAACACAGCTAGAAGCCAGTGCGGATAGAGAGTAGGCTATGATGTGCAAAGG
TTANACACTGGGAGAGACAGGTCCATGAGAGTAGCTTGGACTAACACAGGGAGGGT
TTGGAATCCCAACTGGGGAACCTANAAATCAA

35

Sequence ID 461
TAGGAGGCTTATTCACTGATTTCCCCTATTCTCAGGCTACACCCTAGACCAAACCT

- 159 -

ACGCCAAAATCCATTTCACTATCATATTCATCGGCGTAAATCTAACTTTCTTCCCA
CAACACTTTCTCGGCCTATCCGGAATGCCCCGACGTTACTCGGACTACCCCGATGC
ATACACCACATGAAACATCCTATCATCTGTAGGCTCATTCATTTCTCTAACAGCAG
TAATATTAATAATTTTCATGATTTGAGAAGCCTTCGCTTCGAAGCGAAAAGTCCTA
5   ATAGTAGAAGAACCCTCCATAAACCTGGAGTGACTATATGGATGCCCCCACCCTA
CCACACATTCGAAGAACCCGTATACATAAAT

Sequence ID 462
TCTTTATCAAGTTGAGAAAGTTCCTCCCCTCTATTCCTAGTTTGCTAAGAGTCCTT
10   CTATCCTATTTCTTAATGGTTTAGTAGATGACTCTGTGGTACTTTGAAGGTTGTTT
GCAGAATTTCCATGCCATAGGCAATTTACCTTTCCTTGACATTTGAAGGATTGATG
TTGGTGCCAAGTATAGAATCTTCACAGAGTCCTCCTGTAGCTTCTAAAGGTTTAGC
TTGAAAATGTTAATTGCTTAACGCTAGTAAGTGAGTGAAAAAGCTGGGGATAAATT
TTGTATCTTGCTTATATTTCAGTTCCCACCTCTGTCCNGACNAAACCCCCATATAT
15   AA

Sequence ID 463
TAGTTTACATATCCCAACCTTTAAAAATATTCCTCTTATTAGCTTTATATTCACTT
TATAGAAGTTGAGTTTTAATTAAAATTCTTGGCATCCTGAAGTATGTCACATAGCA
20   TGTGCTCCTTATAAATATGTTGATATCTCAGAAGACAGCATCCCGGTTTTCATTTT
ATAAAGTACCATACTTAAGAATGCTGTAATACTTATCTTTTATAACATGTTTCCTT
CGCTTTGCTTGNCTTTTATGNCATCAGTTTTAACTGTTTACTTCATTTAACAGNTT
ACATCATNCAACAGTTTACTTCATTAAACAGTAGGTGGAAAAATAGATGCCAGTCT
ATGAAAATCTTCCCATCTATATCAAAATACTTTCAAGGATATACTTT

25
Sequence ID - 464   nt: 615
CGACTTTCAACCATCAAGTGAGGAATACCTTCACATAACTGAGCCTCCCTCTTTAT
CTCCTGACACAAAATTAGAACCTTCAGAAGATGATGGTAAACCTGAGTTATTAGAA
GAAATGGAAGCTTCTCCCACAGAACTTATTGCTGTGGAAGGAACTGAGATTCTCCA
30   AGATTTCCAAAACAAAACCTATGGTCAAGTTTCTGGAGAAGCAATCAAGATGTTTC
CCACCATTAAAACACCTGAGGCTGGAACTGTTATTACAACTGCCGATGAAATTGAA
TTAGAAGGTGCTACACAGTGGCCACACTCTACTTCTGCTTCTGCCACCTATGGGGT
CGAGGCAGGTGTGGTGCCTTGGCTAAGTCCACAGACTTCTGAGAGGCCCACGCTTT
CTTCTTCTCCAGAAATAAACCCTGAAACTCAAGCAGCTTTAATCAGAGGGCAGGAT
35   TCCACGATAGCAGCATCAGAACAGCAAGTGGCAGCGAGAATTCTTGATTCCAATGA
TCAGGCAACAGTAAACCCTGTGGAATTTAATACTGAGGGTGCAACACCCCATTTTC
CCTTCTGGAGACTTCTAATGAAACANATTTCCTGATTGGCATTAATGAANAGTCA

- 160 -

Sequence ID 469

GATTTTTAAAAATACATATAGCAAAAATATTACAGGGTCAGGGGAGACAATTAGAA
TGATATAATTCAAAGTGGATTAAAAAAAAAACTGTCACCCAGAATACAATACCCAG
CAAAGTTGTCCTTCATAAATGAAAGAAAAATNAAATCTTTNCCNAACNA

Sequence ID 471

TCCCGGGAATCTGCAGGATCCGTCGACT

Sequence ID 472

GACAGTGCCCAGGGCTCTGATATGTCTNTCACANCTTGNAAAGTGTGAGACAGCTG
CCTTGTGTGGGACTGAAAGGCAAGATTTGTTCCTGCCCTTCCCTTTGTGACTTGAA
GAACCCTGACTTTGTTTCTGCAAAGGCACCTGCATGTGTCTGTGTTCTTGTAGGCA
TAATGTGAGGAGGTGGGGANACCACCCCACCCCCATGTCCACCATGACCCTCTTNC
CACNCTNACCTGTGCTCCCTCCCCAATCATNTTT

Sequence ID - 473   nt: 694

TGGGCTTTGGGCTGGCTGCAGTCTGTCTGAGGGCGGCCGAAGTGGCTGGCTCATTT
AAGATGAGGCTTCTGCTGCTTCTCCTAGNGGCGGCGTCTGCGATGGTCCGGAGCGA
GGCCTCGGCCAATCTGGGCGGCGTGCCCAGCAAGAGATTAAAGATGCAGTACGCCA
CGGGGCCGCTGCTCAAGTTCCAGATTTGTGTTTCCTGAGGTTATAGGCGGGTGTTT
GAGGAGTACATGCGGGTTATTAGCCAGCGGTACCCAGACATCCGCATTGAAGGAGA
GAATTACCTCCCTCAACCAATATATAGACACATAGCATCTTTCCTGTCAGTCTTCA
AACTAGTATTAATAGGCTTAATAATTGTTGGCAAGGATCCTTTTGCTTTCTTTGGC
ATGCAAGCTCCTAGCATCTGGCAGTGGGGCCAAGAAAATAAGGTTTATGCATGTAT
GATGGTTTTCTTCTTGAGCAACATGATTGAGAACCAGTGTATGTCAACAGGTGCAT
TTGAGATAACTTTAAATGATGTACCTGTGTGGTCTAAGCTGGAATCTGGTCACCTT
CCATCCATGCAACAACTTGTTCAAATTCTTGACAATGAAATGAAACTCAATGTGCA
TATGGGATTCAATCCCCACCATCGATCATAGCACCCCTATCAGCACTGNAAACTC
TTTTGCATTAAGGGATCATTGC

Sequence ID 474

GGCAGCGCGGGGAGCCCGTCGGCGCCGGCGGGCGGGCCGGTTTCGAAGTTGATGCA
ATCGGTTTAAACATGGCTGAACGCGTGTGTACACGGGACTGACGCAACCCACGTGT
AACTGTCAGCCGGGCCCTGAGTAATCGCTTAAAGATGTTCCTACGGGCTTGTTGCT
GTTGATGTTTTGTTTTGTTTTGTTTTTGGTCTTTTTTTGTATTATAAAAAATAAT
CTATTTCTATGAGAAAGAGGCGTCTGTATATTTTGGGAATCTTTTCCGTTTCAAG
CATTAAGAACACTTTTAATAAACTTTTTTTTGATAATGGTTAAAAAAAAAAAAAAAA

- 161 -

A

Sequence ID 475

CATAATAAAAAACAATCAACAAACAGGGAATGGAAAGAAACTTCCTCAGCATGGTG
AAGGCCACATATGAAAATCCCACAGCTAACATCATACTCAATGATGAAAGACTGAA
AGCTTTTCTCCTGAGATCAGGAACAAGACAAAGATGTCACCTTTTGTCACTTCTAT
TCAACTCATTATTGGAAGTTTTTGCCAGAGCAATTAGGTAAG

Sequence ID - 476   nt: 476

CAGAATCTTTTCATAGGCTGAATGTTGCTCCACAATGTGTCCTTTGACTATCTCTG
GCTAATTATTATTTTAATCTCTTCTCAGCTTTTCCAAGAACATAACGTTAACCAAA
GATCTTAGGCCATTCACAACTCTTTTGTAAAAATTAATGTGGATGTGAAACGAGGC
AACAAATCCTGAAGTAGAAAGTTATTCCTGGCCAGGCACGGTGGCTCACGCCTGTA
ATCCTGGCACTTTGGGAGGCCGAGGTGGGTGGATCATGAGGACAGGAGATCGAGAC
CATCCTGGCCAACATGATGAAACCCCATCTCTACTAAAATACAAAAAATTAGCTGG
GCATGGTGACGCGTGCCTGTAGTCCCAGTTACTCGGGAGGCTGAGGCAGGGGAATT
GCTTGAACCTCGGAGGTGGGAGGTTGCAGTGTGCCGAGATCACGCTACTGCACTCC
AGCCTGGCAACAGAGCAAGACTCCATCT

Sequence ID 477

AAACAGAAAGTTTCTTCTAAAGGCATGATTCAGTTAAGTCATTCTTAAGTGTTAAA
AAATTGTGAAAAATGTGCCTGTAATCCCAACACTTTGGGAGGCCGAGGCAGGCAGA
TCACGAGGTCAGGAGATCAAGACCATCCTGGCTAACAAGGTGAAACCCCGTCTCTA
CGAAAAATACCAAAAACATTAGCCGGGCGTGGTTGTGGGCGCCTGTAGTCCCAGCT
ACTTGAGAGGCTGAGGCAGGAGAATG

Sequence ID 478

TTCTTGGGATATTGATGACTACTGTCTGAGAGGTGCTGTGGGGAGATTTTCAGGAT
TGTGTGGTCTTTGAGGGGGGTGTTTTTTTAAGACAACATTGACCACTGTCCACTGT
CCACATGATCATTGTAAAATTGCAATGCCGCATGCTAGTTGGTTACATAAGACATA
ATTCCAGTGATTGAAGGTGGTTACACTGTATGGTGGTGTGTTCAAGATGGCACTGG
CATCTTTGAGCAGAGCCTGGCTATGCAGCATCATTTGAGTTTTTTAAACACCCTAN
AGGTCTGGTTGTTGTTGCTGTTGTCCTTTCCTGTGAAAGTCACAANANAAGTTACA
GTCCAGGTGAACCTGGAGTTTATAGGTTGGTTTTGTTTCTGNTATATATATATATA
TATATATTTTTTTTTTTTTTTTAACATTTACCTGTAGTGCTGTAGCTGTTGATACTA
TCACCTGCATGCTATTTCTAGTGAGTGCTAAATACAGTATGGTCCAATGACAATAA

CAGCCCATGGTACTGCCAG

Sequence ID 479
CATCAGTCTGTTATCCATGCTGACTTTCCGAAGACTTGCAGCTACTGCATTGATAT
CTTTCCTGCCAATAAGCAAAGTGTTGAACACTTCACAAAATATTTTACTGAGGCAG
GCTTGAAAGAGCTTTCAGAATATGTTCGGAATCAGCAAACCATCGGAGCTCGTAAG
GAGCTCCAGAAAGAACTTCAAGAACAGATGTCCCGTGGTGATCCATTTAAGGATAT
AATTTTATATGTCAAGGAGGAGATGAAAAAAACAACATCCCAGAGCCAGTTGTCA
TCGGAATAGTCTGGTCAAGTGTAATGAGCACTGTGGAATGGAACAAAAAAGAGGAG
CTTGTAGCAGAGCAAGCCATCAAGCACTTGAAGCAATACAGCCCTCTACTTGCTGC
CTTTACTACTCAAGGTCAGTCTGAGCTGACTCTGTTACTGAAGATTAGGGAGTATT
GCTATGACAACATTCATTTCATGAAAGCCTTCCANAAAA

Sequence ID 481
CACACTTTCATGATAAAAACAGAACCTAGGAATGAAAAGAAATTATAGCAACATAA
TAAAGACCATATATGAGAAGCCCACAGCTAACATACTGTATGGTGAAAAACTGAAA
GCTCTTCCTCTAAGATCAGGAACAAGGCAAGGATGCCCATTCTTGCCACTTCTATC
GAACGTAGTACTGGAAGCCCTAGCCAGAACAACTAGGCAATAGAAAGAAATTAAAG
GCATCCATNTCAGAAAGGAAGAANCAAATGCTGTCTGTTTAANATGACA

Sequence ID 482
TTTCTATANAAAAAAATTTTTTAAAATAATTGTAAAGTTAGATTTAAAATTGTAAA
ATATAAAATCACAAAGGAATGTACCCAATAAAATGTAAATGCNCCATAAAAAAAAA
AAAAAAAAAAAAAAAAA

Sequence ID 483
CGNTAACGTGCAATCCGCCGCACGCCAGCAAACTGGACAAACTCCGGGATCTCATC
GAAGCGATTGAGCACCAGTACCAGAGTAATACCGGACTGATGTAACGAGGCGAGTC
GCTCATCCAGCTTGCTGACGTGAGGCAACATCCAGGCCATCGAACGGNTCATCAAG
AATCAACAAGTCAGGCTCCGACATCAGCGCCTGACACAGCAGGGTTTTTCGCGTCT
CGCCAGTGGAAAGGTATTTAAAGCGTCNGTCGAGGAGGGCGGTAATACCGAACTGC
TGCGCCAGTTGCATGCAACGCGGTGCATCCTTTACTTCATCCTGAATGATCTCAGC
CGTAGTGCGTCCGGTGCCATCTTCGCCAGGGCCGAGCATATCGGTGTTATTCCGCT
GCCATTCGTCGCTGACGAGTTTTTGCAATTGCTCGAAGGAGAGACGAGTGATGTGG
GAAAACTGGCTTTGCCGTTCACCTTTCAAAAGCGGGAAGTTCCCCCGCCAGCGCGC
GGGCCAGGGCCCGAT

- 163 -

Sequence ID 484

TTTTTTTTTTTTATTCTATTAAAAAATGTTNNTGAAAAAAGATACTTAAATTTTAA

AGATAACTNAATTCCTAANGATTTAAAATAATCCAAGCAGAGATGAAAGANCAAAT

GCAAATGCNTAAAAAGACCCCANAGCATTGTTAGCAAAAAGCAAATATAGTTAGCC

5   AAGCATATATATNTCATAAAAGCAATAANAAGGCNTAAAGCAAGTTTGGGGAGAGC

TTATTTAAAACTTGTAAAAATCATTTGAATTTTTAAAAGTTTTCAAAC

Sequence ID - 485   nt: 551

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10   TAGAAAGATAGAGACAGAGTGATTTGCAAAATAATGGAGGATCATATTTATATATG

AATTTTCACTTATTTGAACTTTCAGATATCANCTTNAAAANCTTTGGTTTAAGTAA

AGTNTNTTAATGAGACTCCTTGGATGAAAGTAACCAAAACCAGTAAAAATAAGGTA

ATAAGGATGTAATAGTTTCTTATGGACACTCAACAGCTAGAATGCAGTTAGTCTCA

GAAAAGAATTAGAACAAATAACTGGAAGGCCATCAGGAGTCCAAAACCATCACTCT

15   TTTATATTTTATATTTTATTTTTCTCTCTTCANATGAGCATTCTCTTTCTATGTCC

ATATGGTANAAGGCGGCAGCTCCATAGATTATGGCTTCAGATGTTACAGTTCCGCT

NAATGCAGGGACAGACTTGCTATCTTTCAGTCCCCTTACATATCCTGGGGAGAGAG

CAAATGATTGACTGGCTTGAGTCAGGTGCCCGTTCCCTTTCCAATCT

20   Sequence ID - 487 nt:224

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ATGTTCTTAGAAGCANGAAAAAGAATTCAGNTTTGCTTTGTATACTAAATTAAATG

CTGTAATTTTGATAAAATGAAAAATCTGCTTTATTTGCAACAATTGGTTTCTTCCT

TGACGTCAGCCTCACTCTTGGACTTTGGTATTCAGCCNGNCACCCCTGGGAATTCC

25

Sequence ID - 488   nt: 349

GTGCCTCCCTGTGTGAGTAGCCTAAGGTGCATTGAAAAGACTGGGATGTGTTTTA

TTTTTTTGTATTAGATAGCATTAACCTTACTGTTGAAGTATTTTTGGTGGAGTATT

AGTGACAAGCCATTGAGTCTTAAGCCTTACGGCTTCCTATAAAATCACTAATTTCG

30   TGTGTGTTTGTGTGTAGGTTACGTTATATATAGGATTCGTGTTCGCCGTGGTGGCC

GAAAACGCCCAGTTCCTAAGGGTGCAACTTACGGCAAGCCTGTCCATCATGGTGTT

AACCAGCTAAAGTTTGCTCGAAGCCTTCAGTCCGTTGCAGAGGANCGAGCTGGACN

CCCTGGGGGGCTC

35   Sequence ID 489

TTAACAGCTGCATAGAGTTTTAAAAGTACATTATATTTTGTCAGACAAGTAAAATA

TCTGTTTTTCACGCAAAAAAAGCCATGAAATACGTAATTTTTTAAAGACAAAAAAT

- 164 -

CATCTTTTGAGTTTGCTCTTTGGTTTTTCTTCATTCCTTTTGAGGATTGGGAAAAC
AGAAAGATTCTTTGATTTGGGTAATGAAGAGGTAATTTGGGACAGTGTGGTGGTAC
CAGGAAGAAAGAGGATTGGAAAGGCCAGTACTGTTTTAGTTGCTCGGCACTGTTGG
TTTTGTTTTAATGTGGTTGCCCTGTCCACTACATGGTTCTATCAGTAGTGTAATCC
5 ATTTTCAATGTAAAGCTCTTTTAGTTTTTGTCATAGACATAAATTAATATTTTGAG
AGGCATCCCTCACCTGTTCATTTCTTCTGTGTTGAAATGAAGTACTTAAAATTACC
GTTATACATGAACTTTGTGGACTGTAAGATTTGTTATATATGTTCAAATGCCTTTT
AGCTGGCTTTTTAATTAATATGCCTGTTTTGAGTGCTTAATACAATGTAATGNGGA
TTGTAAATCATACCTATTTTAAATCATTCCTTCCTGTATATTTGNACTCAGAGAGC
10 CTTATTTTATTCTTCCAGC

Sequence ID - 491   nt: 382
TTTTCTTAGAACTTTATTTTTTCTGGCCAGGCGCAGTGGCTCACACCTGTAATCCC
AGCACTTTGGGAGGCCAAGGCAGGTCGATCACCTGAGGTCAGGAGCTCAAGACCAG
15 CCTGGCCAACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCTGGGCG
TGGTGGCGCATGCCTGTAATCCCANCTACTCAGGAGGCTGAGGCAGGAGAATTGTT
TGAACCCGGGAGGCGGAGGTTGCANTGAGCCGAGATTGCGCCACTGCACTCCAGCC
TGGGCAACAGAGCGAAACTCCATCTCAAAAAAAAAAAAAAAAAAACAACCTTTATTT
TTTCTGATTTTAAAAGTAATAACTAGTTTGTAGAAACATTAAAAGT

20

Sequence ID 492
ACCCTAAACATAACTTAAAATTTGTTNGGAATTTGAAAGTACAGAATTTTCCTGTA
ATTGAGACTNTTTAAACTTTTGTGGTTGGAGAAGGTATTCTATTTTTTGAAAATAT
CTGTAAGTTTTATCTAAATAGTAAACTCTAAGTATTCTTCCCCTTTACTTACAGCC
25 ACCCTGGGAATCTGAGACTAGAGAAAATAAAGTTTGTCTCTTGTTCTAAGGAGGGT
CTGGTTTAGAAATCTGATTTAGACATAGAAAAATTGCAAGAAGCTTGAGGTGATTG
GAAGATACGATTTTGTTATCAAAGNATGTTTCTGTTTTATAGATTTTATTCATCTA
CAACTCCTTATTAATATATTTAAGAAGTCATTAACCCACCATTGATTACTTGATAT
AAAAGGAGAANCGGTGGTAAAAGGTGAAATANAATTTTTAATTTTTTTTTTTTTAA
30 GTTTAGGATTTTTTTTTAAATTCTAAGAGTTTCTGTCATTTGGGGACAATCAGAA

Sequence ID 493
TGGGAATCATAATTNGTTAACTGAAGCTNATAAGATGAGAGCATTCANAGAGAAAA
GAACGGAAAGATTGAATATCAGTTTCCCTTCTTTAAAAAAATTGTGGATATGTGAT
35 CTAGCTTCTTGAGCATCACAGTGACTGATTGGCTCGTGGTAATTGATCGCTATGCT
GACAATCTTATCTCCACCTATGTCATTCAATTTTCTAAGAGGCAAAATCCTTAATC
AGGAGGAGAGTTTAGCTCTAGCTAAATTTCCCTTGTCCAGCATGCTCCTGCTCCCC

- 165 -

CAACTTGTGGAAACAGCTAAAGGATTGGACTAGGAGCANAAGTTTGGAATGGTTAA
AATGTAGCAACATGTGTTTCCTGAAACAAAATTCCACTATAATAAAAAAAGCATTT
GAATGCTCCCTTGTAATTCTGTTGGAGCTTGTTGCCTTTTTTATGACACAACCATA
ATCAGTGATAGACAGTAGCATAAAGAAGCAAGAGCAAAGCAATTAAGTAATAATAG
5   CACTACAAAAATGTGTGCTGTACTTACCAAACACGACATTTATGAATTATTANATA
GGAATAAGGGGATGGT

Sequence ID 494

10   GACCCAGCCATCTAAATAAGTTRTACATGTTGCGTATTTTTTTGTTAGGGACTTAT
CTTCCGAAGAGGAAAGGTTTATGAAACCTAAAGTAACAATGATAGCTTGGAATCAA
AATGATAGCATTGTTGGCACAGCTGTGAATGATCATGTCCTCAAAGTGTGGAATTC
TTACACTGGACAACTGCTTCATAACTTAATGGGACATGCTGATGAAGTATTTGTTC
TGGAGACACATCCCTTTGATTCCAGAATTATGTTATCTGCAGGACATGATGGCAGC
15   ATATTTATATGGGATATTACAAAAGGTACCAAGATGAAACATTATTTTAATATGGT
AAGTGAAGTGAGATGTACCTTGATACATGCTTGATAATTTGTTTAGAGTATTTGGG
TTATGCGGCTTACCCAGAAATTGATCTGCTTGTTTTGGCAGTTTGTTTTTACAAAT
CAACATATTCAAAGCCTGCTAAATATTAGACAGCTACATGTATATACGTACATACA
TGAA
20
Sequence ID 495
TTTC

Sequence ID 496
25   CTCGCTGGCGGGAGGCCACGGGCTTTCCACAGCGCGGGGGAACGGGAGGCTGCAGG
ATGGTCAAGCTGACGGCGGAGCTGATCGAGCAGGCGGCGCAGTACACCAACGCGGT
GCGCGACCGGGAGCTGGACCTCCGGGGGTGATCTGGACCCTCTGGCATCTCTCAAA
TCGCTGACTTACCTAAGTATCCTAAGAAATCCGGTAACCAATAAGAAGCATTACAG
ATTGTATGTGATTTATAAAGTTCCGCAAGTCATAGTACTGGATTTCCAGAAAGTGA
30   AACTAAAATTTTAATCCAGGTGCTGGTTTGCCAACTGACAAAAGAAAGGTGGGCC
ATCTCCAGGGGATGTAAAAGCAATCAAGAATGCCATAGCAAATGCTTNAACTCTGG
CTGAAGTGGANAGGCTGAANGGGTTGCTGCAGTCTGGTC

Sequence ID 497
35   GAAGACCTCACATCTGAGAGCTCATCTGCGTTGGCATTCTGGAGAACGCCCTTTTG
TTTGTAACTGGATGTACTGTGGTAAAAGATTTACTCGAAGTGATGAATTACAGAGG
CACAGAAGAACACATACAGGTGAGAAGAAATTTGTTTGTCCAGAATGTTCAAAACG

CTTTATGANAAGTGACCACCTTGCCAAACATATTAAAACACACCAGAATAAAAAAG
GTATTCACTCTANCAGTACAGTGCTGGCATCTGTGGAAGCTGCGCGAGATGATACT
TTGATTACTGCAGGAGGAACAACGCTTATCCTTGCAAATATTCAACAAGGTTCTGT
TTCAGGGATAGGAACTGTTAATACTTCCGCCACCAGCAATCAAGATATCCTTACCA
5   ACACTGAAATACCTTTACAGCTTGTCACAGTTTCTGGAAATGAGACAATGGGAGTA
AATATTACACAAATACTTATTCATTGNGGTTATTTTTATACAGTAGTGAGAAGAAT
ATTGTTCCTAAGTTCTTAGATATCTTTTTTTGGATGTGCAAAAATTTTTGGATTGA
CAGTAACTTGGGTATACATGACACTGAAATGCCTTACTTTGGATGA

10   Sequence ID 499
TGCCTGCGGGCCAGGACCTCGCCCAGCCCATGTTCATCCAGTCAGCCAACCAGCCC
TCCGANGGGCAGGCCCCCCAGGTGACCGGCGACTGAGGGCCTGAGCTGGCAAGGCC
AAGGACACCCAACACAATTTTTGCCATACAGCCCCAGGCAATGGGCACAGCCTTCC
TCCCCANAGGACCCGGCCGACCTCAGCGCCTCCTGCAGGCTAGGACACTGGTGCAC
15   TACACCCCATGCCTGGGGGCCGAGATTCTCCAGCAGAAAGATGCAATATTTTTTGT
TTCCTTTTTTTTCCATTTTTTTTCTCTAAGGAATCAATATTTCAATATGTTGAGTGTG
TGTCCAATGCTATGAAATTAAAATATTAAATAACATATTTATGGCATTTTCTTGAA
GAGTGTGGTTGAAGAAATATTTCTCCTTTTGTTTTTCTTTTTTTTTTTGNTTGNTAC
TGCCACTTCTTTTTAGGAGCAAATCTCCCCAGGGGTGTACGGNATTTCTTGACTCT
20   GGAACAGCTGCTACCCCCAAGACTTGCCACGTTGTTCTGCCCTCAAATGGAATTA
AGTG

Sequence ID - 500   nt: 390
GGAATATGGTCAGGATCTTCTCCATACTGTCTTCAAGAATGGCAAGGTGACAAAAA
25   GCTATTCATTTGATGAAATAAGAAAAAATGCACAGCTGAATATTGAACTGGAAGCA
GCACATCATTAGGCTTTATGACTGGGTGTGTGTTGTGTGTATGTAATACATAATGT
TTATTGTACANATGTGTGGGGTTTGTGTTTTATGATACATTACAGCCAAATTATTT
GTTGGTTNATGGACATACTGCCCTTTCATTTTTTTCTTTTCCAGTGTTTAGGTGAT
CTCAAATTAAGAAATGCATTTAACCATGTAAAANATGANTGCTAAAGTCAGCTTTT
30   TAGGGCCCTTTGCCAATAGGTANTCATTCAATCTGGTATTGATCTTTTCACAAA

Sequence ID 502
ACCCGCCATCTTCCAGTAATTCGCCAAAATGACGAACACAAAGGGAAAGAGGAGAG
GCACCCGATATATGTTCTCTAGGCCTTTTANAAAACATGGAGTTGTTCCTTTGGCC
35   ACATATATGCGAATCTATAAGAAAGGTGATATTGTAGACATCAAGGGAATGGGTAC
TGTTCAAAAAGGAATGCCCCACAAGTGTTACCATGGCAAAACTGGAAGAGTCTACA
ATGTTACCCAGCATGCTGTTGGCATTGTTGTAAACAAACAAGTTAAGGGCAAGATT

- 167 -

CTTGCCAAGAGAATTAATGTGCGTATTGAGCACATTAAGCACTCTAAGAGCCGAGA
TAGCTTCCTGAAACGTGTGAAGGAAAATGATCAGAAAAAGAAAGAAGCCAAAGAGA
AAGGTACCTGGGTTCAACTAAAGCGCCAGCCTGCTCCACCCAGAGAAGCACACTTT
GTGAGAACCAATGGGAAGGAGCCTGAGCTGCTGGAACCTATTCCCTATGAATTCAT
GGCATAATAGGTGTTAAAAAAAAAAATAAAGGACCTCTGGG

Sequence ID - 503   nt: 109
ACATTTTCCGGNCCTTTTGCCATACACAGTTACAGAGATCAGTCAAATCCATACCA
CCACTGAGATCTCATTTATTGCCACAGATGCACAAAATAAATAACCCAAAATC

Sequence ID - 504   nt: 374
CCAGCAACGACCCATACCTCAGACCCGACGGCCCGGAGCGGAGCGCGCCCTGCCCT
GGCGCAGCCAGAGCCGCCGGGTGCCCGCTGCAGTTTCTTGGGACATAGGAGCGCAA
AGAAGCTACAGCCTGGACTTACCACCACTAAACTGCGAGAGAAGCTAAACGTGTTT
ATTTTCCCTTAAATTATTTTTGTAATGGTAGCTTTTTCTACATCTTACTCCTGTTG
ATGCAGCTAAGGTACATTTGTAAAAGAAAAAAACCAGACTTTTCANACAAACCC
TTTGTATTGTANATAAGAGGAAAAGACTGAGCATGCTCACTTTTTTATATTAATTT
TTACAGTATTTGTAAGAATAAAGCANCATTTGAAATCG

Sequence ID 505

GTACAGGAGGTAAATTGGATACCCCATCTAAGGGGATCTGTGAGACCAGGTAGTTA
TTTGGAATGAAAGAGTAAGATATTAAACCAGCCAGCATGTCAACAGGTGGGTGATA
GTCTTGTTCTCACAGACAACAGATGGCCATCATCTTAAAACAACATTTATGTTAAC
CAGCAGATAAGGGACTCCTGCATTGTCAGTGGACTTTGAGCCTGAGTTTTTCTACT
TGCATAGGTGAAAGTGGACTGCAATGCTAGTATAAATGCCGTATGATGACTAGTAC
CCCTTAGGGAGCTCCAGTTTGCCTTCCTGGGGAACCACAGACCCCAAGTGTAATTT
CCTGAGGACAGCCCGACTTCT

Sequence ID 506
GTTACTGTGAGCCTGTCAGTAGTGGGTACCAATCTTTTGTGACATATTGTCATGCT
GAGGTGNGACACCTGCTGCACTCATCTGATGTAAAACCATCCCANAGCTGGCGAGA
GGATGGAGCTGGGTGGAAACTGCTTTGCACTATCGTTTGCTTGGTGTTTGTTTTTA
ACGCACAACTTGCTTGTACAGTAAACTGTCTTCTGTACTATTTAACTGTAAAATGG
AATTTTGACTGATTTGTTACAATAATATAACTCTGAGATGTGTGAAAAAAAAAAAA
AAAAAAAAAAAA

Sequence ID - 507   nt: 521

CTGCGGTGGAGCCGCCACCAAAATGCAGATTTTCGTGAAAACCCTTACGGGGAAGA
CCATCACCCTCGAGGTTGAACCCTCGGATACGATAGAAATGTAAAGGCCAAGATC
CAGGATAAGGAAGGAATTCCTCCTGATCAGCAGAGACTGATCTTTGCTGGCAAGCA
GCTGGAAGATGGACGTACTTTGTCTGACTACAATATTCAAAAGGAGTCTACTCTTC
ATCTTGTGTTGAGACTTCGTGGTGGTGCTAAGAAAAGGAAGAAGAAGTCTTACACC
ACTCCCAAGAAGAATAAGCACAAGAGAAAGAAGGTTAAGCTGGCTGTCCTGAAATA
TTATAAGGTGGATGAGAATGGCAAAATTAGTCGCCTTCGTCGAGAGTGCCCTTCTG
ATGAATGTGGTGCTGGGGTGTTTATGGCAAGTCACTTTGACAGACATTATTGTGGC
AAATGTTGTCTGACTTACTGTTTCAACAAACCAGAAGACAAGTAACTGTATGAGTT
AATAAAAGACATGAACT

Sequence ID 508

AAGCTCATGATTTTAAATGTATTTTTCTAATAAACTATACTCCCATTTAAAAATCA
CCAATACCTTAATGTTTCAATTATATAAGCTAATTAAAAATAAAGGCTGGGCGTGG
TGGCTCACTTTGGAAGACCGAGGCAGGCAGATCACCTGAGGTCAGGAGTTCGAGAC
CAGCCTGCCCAACATGGAGAAACCCCATCTCTACTAAAAATACAAAATTAGCCAGG
CATGGTGGCACATGCCCGTAATCCCAGCTACTGGGGAAGCTGAGGCAGGAGAATCA
CTTGAACCTGGGAGGCAGGGGCTGCAGTGAGCCGAGATCATGCCATTGCACTCCAG
TCTGGGCAACAATAGTGGAACTCCATCTCAAAAATAATAAAAAAAATAAAATAAAA
ATAAAATTCAAACCTAAAATAGATGCTCTACTTCAGGAGTGGGCAAATTAATCACC
TGCATCCTTTTTTTGGGCTTTC

Sequence ID - 509   nt: 575

TTTTTTTCTAAATGGNGATTACTAATATATGTGGAGACTATTAATCTCTTTTCTGT
TGCCATTAGTTCATTTTTCCCCAAAAGCCAATACATGTTCATTACAAAAATGAATT
ATAAAATATAAGTTAAAAGAAAAACATAAAACCCTACAATCTTACCCACCCAGACA
ACTACTATTAATACCTTAGTATTAACATATACACATCATGTATATGTATAAATTTA
TCTTAAACAAAAATAAAATTATTCTTTACATATTGTTTTAAAACCTATTTATCTGG
CCAGGTGCCGTGGCTCACGCTTGTAATCCCAGCACTTTGGGAGGCTGAGGCACGTG
GATCACCTGAGGTCAGGAATTCGAGACCAGCCCAGCCAACATGGTGAAACCCTGTC
TCTAATGGTTTAAATACCAAAAAATTAGCTGGGCATGGTGGCACATGCCTGTAATA
TCAGCTAACATGGGAGGCTGAGGCAGGAGAATCACTTGAACCANGGAGGGGGAGGT
TGCAGTGAGCCGAAATCACACCACTTCACTGCAGCCTGGGCAACAAAGCAAGACTG
TCTCAAAAAGAAAAA

Sequence ID 510

CACTGTCATTCCCAGGAGGCTTTGGAGTCAGAACTGGATTCAAATTCTGACTNTAT
GTTGTGTGACTTGGGCCAATAGCTTCTTTNTGTGCCTCAGTTTCTTTAGCTGTAAA
TANACGGGTAGGTCACCCCTTACCCCATAGGTTATGGGGAAAGTTACAGAAAATGG
TCAGCTGGGCNCAGTGGCTCAAGCCTGTGGTCCCAGCNCCTTGGGAGGCCAAGGTG
AGCAGATTGCTTGAGCCCAGGAGTTTGACACCAGTNTGGCAACGTGACGAAACCCT
ATCNCTGTGAAAAATACAAAAAATTAGCCAGGCATGGTGGTGTGTGTCTGTGGTTC
CAGCTGCTTGAGAGTTTGAAGTGGGAGGATCACCTGAGCCCAGAAGGTCGAGGCTG
CAGTGAGCTGTGATCGCGTCACTGCACTCCAGCCTGGC-GACAGAGTGAGA-CCCC
T-TTTGAAAAAAAAAAAAAAAAAAAT

Sequence ID 512
GTGAGCGGTGGTGGTTTATTCTTCCGTGGAGTTAAGGGCTCCGTGGACATCTCAGG
TCTTCAGGGTCTTCCATCTGGAACTATATAAAGTTCAGAAAACATGTCTCGAAGAT
ATGACTCCAGGACCACTATATTTTCTCCAGAAGGTCGCTTATACCAAGTTGAATAT
GCCATGGAAGCTATTGGACATGCAGGCACCTGTTTGGGAATTTTAGCAAATGATGG
TGTTTTGCTTGCAGCAGAGAGACNCAACATCCACAAGCTTCTTGATGAAGTCTTTT
TTTCTGAAAAAATTTATAAACTCAATGAGGACATGGCTTGCAGTGTGGCAGGCATA
ACTTCTGATGCTAATGTTCTGACTAATGAACTAAGGCTCATTGCTCAAAGGTATTT
ATTACAGTATCAGGAGCCAATACCTTGTGAGCAGTTGGTTACAGCGCTGTGTGATA
TCAAACAAGCTTATACACAATTTGGAGGAAAACGTCCCTTTGGTGTTTCATTGCTG
TACATTGGCTGGGATAAGCACTATGGCTTTCAGCTCTATCAGAGTGACCCTAGTGG
AAATTCGGGGGATGGGAAGGCCACATGCATTGGAAATAATANCGCTGCAGCTGTGT
CAATGTTGAAACAAG

Sequence ID 513
TTTTTTTTTTATAAACTCCAATCATTTCCAGAGCTACTTAGCTCAGCATCTTTTTT
TTCCACGCTCTTAAGTTGTGTTTATACATTTTTGATACAGTTAGATTGTTTTTGTC
ACATTCTTCATTCTATCCTGGGATCCCCCAACCACCTAAGTGGATTTTTTGATAAT
TTGCATGCTTTAAGGATAACTCTTCATTCTGNAAAGGGCTATGGGTTTTGGCAAAT
GCAGAGTCATGTATCCAAGATTACAATATCGCACAGAAGAGTTTCATCACTATATA
AAACTCACCAGTCTTCCTCCTATTCAACCATCTCCATGCCTTCTTCCCAGCCCTAA
CTCCTTAAAACCACTCATATCTTTACTATTGCTATAGTATTGCCTCTTCCACCATG
TCATATAAATGGAAACATACAGTATTAGTCTTCTCAAACTAGTTTCTTTTACCTAA
CAACATGCATTTAAGATTCATAGTGTCTTTTAATGACTTGATAGATTATTTCTTTG
TAGCTGAATAATATTGCATCTTATAGATGTAACCGTTTGTATATCCATATTTTCTC
ACAGCCTATGACTTGNCTTTTGATTCTCTGAACAGGCCATTCACAAAGCAGAAGTT
TTAATTTTTATAAAGCTAATGNATCAACTT

Sequence ID 515

CCTGGATGACAGCATATCTGTTTATAGCTCAGTTTACTGAATACTTTAAGCCCACT
GTTGAAACCTGCT

5   Sequence ID - 518   nt: 502
        GATGCATGTCCAGCATAGGCAGGATTGCTCGGTGGTGAGAAGGTTAGGTCCGGCTC
        AGACTGAATAAGAAGAGATAAAATTTGCCTTAAAACTTACCTGGCAGTGGCTTTGC
        TGCACGGTCTGAAACCACCTGTTCCCACCCTCTTGACCGAAATTTCCTTGTGACAC
        AGAGAAGGGCAAAGGTCTGAGCCCAGAGTTGACGGAGGGAGTATTTCAGGGTTCAC
10   TTCAGGGGCTCCCAAAGCGACAAGATCGTTAGGGAGAGAGGCCCAGGGTGGGGACT
        GGGAATTTAAGGAGAGCTGGGAACGGATCCCTTAGGTTCAGGAAGCTTCTGTGCAA
        GCTGCGAGGATGGCTTGGGCCGAAGGGTTGCTCTGCCCGCCGCGCTAGCTGTGAGC
        TGAGCAAAGCCCTGGGCTCACAGCACCCCAAAAGCCTGTGGCTTCAGTCCTGCGTC
        TGCACCACACATTCAAAAGGATCGTTTTGTTTTGTTTTTAAAGAAAGGTGANAT
15

        Sequence ID 519
        CTGCGATNGAGTTTTGAGAGGAAGGANTAAAGTNCTCATCTCNGACGGTGAGAAAG
        ATCATNACTAAGGAAACGCAGGGTTGGAAGCAGTGCTGANTGTCCAGTTGAGTTTC
        ATGANCAAACATTTGCTGTGGGACCAGTTTTCATGGNGGTTTGTCATTTTGTCCAG
20   CTGCCTGGAGCTGCTTGGTTGAAGGCACAGAATAATCAGGATTAATTGTTNAACTT
        GTATGAATTTCTTTATTTTAAAATAGGAATAATATCTGCCTTGGGAGCAAGTTGTA
        AGAGTTAACTGAAAGCTTNAGGAAAAACTTTCCCTTGCTATTTAAGTAGGGCTTTA
        CAAGTTACAATTCTATCACAGTTTTAAGATTATAAAC

25   Sequence ID 521
        GCGGCGCANCTGCGGATCCANAAGGNCATAAACGANCNGAACCTGCCCAANNCGTG
        TGATATCACCTTCTNAGATCCAGACNACCTCCTCAACTTCAAGCTGGTCATCTGTC
        CTGATGAGGGCTTCNACAAGAGTGGGAAGTTTGTCTCAAAAAA

30   Sequence ID - 523   nt: 585
        GATTTACTGTGGGAATTTGCTCATGCAATTATGGAAACCTAGAAGTCCCATAATAT
        GCCATCTTCAAGCTGGAATCCCAGGAAAGCAGGTGGTGTAATTCTGAGATTGAAGT
        CTTGAGAACCGGGGGAGTCAATGGTGTAACTCCCAATCTAGGGCTTAAGGCCCAAG
        GACCAGGGCTGCTGGTGTGCAGATGCAAATCCTGGAGTTCAAAGGATTGAGAACCA
35   GGAGCTCTGGTGTCTGAGGGCAGTAGAAGATGGATGTTCCAGCTCAAGAAGGGAAA
        GTAAGAATCCGTCCTTCCTCCACTTTTTTGTTCTATTCAGATGAGCCCTCAATGGA
        CTGAACGATGCTCACCCACACTGTGAGGGCTGGTCTTCTTTATTCAATCCACTGAG

TTAAGTGCTGATCTCTTCTGGAAACACCTTCACAGACACACCCAGAAATAATGTTC
TACCAGCCATGGGCCTGTTACTTAGCCCAGTCAAGTTGACACAGAAAATTAGCTAT
CACAACATCTGTGTGTGTATATACATATGTATTTGCATGTGTGTGTATATATGGNG
TATATATATTCATGTGTGTGTATAT

Sequence ID 524

CTTTTGCCAGTAGGCCCCCTGAGTAGGTTCCTCTATCTTTTGGCATGACCCCAGAA
GTCTTTGATAACTTCCTTGCTTTCTGATGTGACAAGACATCCAGGGCCAGATTGTC
CATATCCTGCCCCGGATGCACGATGCACTGTTTCTCCAAGAATCCCTGTGTCCTTT
GCTGATGATGCCATGATTTTAAGTTCTCTAATATAGTTTTATCTCTTTGTTTCAGA
TAATGCTTTTGTGTTCTCACATGTCCTGCTCTCTCTCTCTCTCATTTTGGTGTT
GATCAGTCTTTCCATAAGATTGTTTATTTCACTAGTCCTTCATTCTTCTTTTTTCT
AAATTTACTCTTCTTGACTAGTATCCTGTCACTTCTGAGGACTCATATTTTTGCAA
CTTGAAAATTATTCTTATTTATTTAAGTATATGTTNCTGAAACTCTCATTAGACAC
ATTTTG

Sequence ID 525

GTTAAAAAAAGTAAAAGGAACTCGGCAAATCTTACCCCGCCTGTTTACCAAAAACA
TCACCTGGTAGCATCACCAGTATTAGAGGCACCGCCTGCCCAGTGACACATGTTTA
ACGGCCGCGGTACCCTAACCGTGCAAAGGTAGCATAATCACTTGTTCCTTAAATAG
GGACCTGTATGAATGGCTCCACNAGGGTTCANCTGTCTCTTACTTTTAACCAGTGA
AATTGACCTGCCCGTGAAGAGGCGGGCATAACACAGCTGAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAATTTT

Sequence ID - 526   nt: 516

CTTTTCATGGTCTCTTGTTCATTAATCATCTAAAATCCAAGCNCAGAGAATTCAAT
TTTAGATGGTCTCCAGAGCAGAATTTGATGTATAATCTTAATTACAAATCATAGAT
AATTAATATTGNTTACAAAATCANAATACGATTAGAGGTAGGGATCCTGCACACAC
CCTATTTTCCTCCCCAGTGTTCTGACCGAGAGACTAATTAATAATTCAAGGAACTT
ACAGTGAATGANAACCCATGGTTTTGCTTAATTATCAGAACAGCTAGATCTGAGAA
CAGCTGTCTCCCACATGGATAGACACTTATTCCACCCATTTGCAGGTAGAATAGCT
GGCAATAATAAGTCCTTCCCATTGGATATGTTGAAAGGTGCCTGCCATGGCATAGT
TGCCACAAGAGAGGAAGAAATGGACACAAATGTAGGCTGTTTTCAGGGCANAGGGA
AGGTGGGAGGAAACCAANTTGCTGGTTTTCACACACCCTCTGGGGAACACCCATGC
ACCTATGANATG

Sequence ID 527

GACAAAAGCTGAGAGAATTTTTTTCTTGAATATTTGCACTAAAAGATAGGTTAAAA
TTCTTCAGGCTGAAGAGAGCATACCAGGTGGAGATTTGGATCTACAAAAAGGAAGG
AAGATTTGGAAATGGATTTGGCACCATTGACTCAATTTCCAGAACAAGAAAGCAGG
GACAGTTTTGGGAAGCTCAAGACACACTGCCCATGAGCAGCAATTTGGACCTCCTG
CTGCATCCACTGTGCATCAAACACACACTGTACAGACAAAGACTCCCAGGAAAAGA
AGTATAAACATGGACTAACACAGAGATGGGCAAACTACAGCCTGTGACCCAGCCAC
CTGTTTATGTAGAATCCAAAGTAAGAATCTTTAACTTACACATAAACTT

Sequence 529; 660nt

GACAGCAGAGCACACAAGCTTNTAGGACAAGAGCCAGGAAGAAACCACCGGAAGGA
ACCATCTCACTGTGTGTAAACATGACTTCCAAGCTGGCCGTGGCTCTCTTGGCAGC
CTTCCTGATTTCTGCAGCTCTGTGTGAAGGTGCAGTTTTGCCAAGGAGTGCTAAAG
AACTTAGATGTCAGTGCATAAAGACATACTCCAAACCTTTCCACCCCAAATTTATC
AAAGAACTGAGAGTGATTGAGAGTGGACCACACTGCGCCAACACAGAAATTATTGT
AAAGCTTTCTGATGGAAGANAGCTCTGTCTGGACCCCAAGGAAAACTGGGTGCANA
GGGTTGTGGANAAGTTTTTGAAGAGGGCTGAGAATTCATAAAAAAATTCATTCTCT
GTGGTATCCAAGAATCAGTGAAGATGCCAGTGAAACTTCAAGCAAATCTACTTCAA
CACTTCATGTATTGTGTGGGTCTGTTGTAGGGTTGCCAGATGCAATACAAGATTCC
TGGTTAAATTTGAATTTCAGTAAACAATGAATAGTTTTTCATTGTACCATGAAATA
TCCAGAACATACTTATATGTAAAGTATTATTTATTTGAATCTACAAAAAACAACAA
ATAATTTTTAGATATAAGGATTTTCCTGGATATTGCACGGGAGA

Sequence ID 529

GACAGCAGAGCACACAAGCTTNTAGGACAAGAGCCAGGAAGAAACCACCGGAAGGA
ACCATCTCACTGTGTGTAAACATGACTTCCAAGCTGGCCGTGGCTCTCTTGGCAGC
CTTCCTGATTTCTGCAGCTCTGTGTGAAGGTGCAGTTTTGCCAAGGAGTGCTAAAG
AACTTAGATGTCAGTGCATAAAGACATACTCCAAACCTTTCCACCCCAAATTTATC
AAAGAACTGAGAGTGATTGAGAGTGGACCACACTGCGCCAACACAGAAATTATTGT
AAAGCTTTCTGATGGAAGANAGCTCTGTCTGGACCCCAAGGAAAACTGGGTGCANA
GGGTTGTGGANAAGTTTTTGAAGAGGGCTGAGAATTCATAAAAAAATTCATTCTCT
GTGGTATCCAAGAATCAGTGAAGATGCCAGTGAAACTTCAAGCAAATCTACTTCAA
CACTTCATGTATTGTGTGGGTCTGTTGTAGGGTTGCCAGATGCAATACAAGATTCC
TGGTTAAATTTGAATTTCAGTAAACAATGAATAGTTTTTCATTGT

Sequence ID - 530   nt: 660

GACAGCAGAGCACACAAGCTTNTAGGACAAGAGCCAGGAAGAAACCACCGGAAGGA

ACCATCTCACTGTGTGTAAACATGACTTCCAAGCTGGCCGTGGCTCTCTTGGCAGC
CTTCCTGATTTCTGCAGCTCTGTGTGAAGGTGCAGTTTTGCCAAGGAGTGCTAAAG
AACTTAGATGTCAGTGCATAAAGACATACTCCAAACCTTTCCACCCCAAATTTATC
AAAGAACTGAGAGTGATTGAGAGTGGACCACACTGCGCCAACACAGAAATTATTGT

5 AAAGCTTTCTGATGGAAGANAGCTCTGTCTGGACCCCAAGGAAAACTGGGTGCANA
GGGTTGTGGANAAGTTTTTGAAGAGGGCTGAGAATTCATAAAAAAATTCATTCTCT
GTGGTATCCAAGAATCAGTGAAGATGCCAGTGAAACTTCAAGCAAATCTACTTCAA
CACTTCATGTATTGTGTGGGTCTGTTGTAGGGTTGCCAGATGCAATACAAGATTCC
TGGTTAAATTTGAATTTCAGTAAACAATGAATAGTTTTTCATTGTACCATGAAATA

10 TCCAGAACATACTTATATGTAAAGTATTATTTATTTGAATCTACAAAAAACAACAA
ATAATTTTTAGATATAAGGATTTTCCTGGATATTGCACGGGAGA

Sequence ID 532

GAATTGTGATAGTTCAGCTTGAATGTCTCTTAGAGGGTGGGCTTTTGTTGATGAGG

15 GAGGGGAAACTTTTTTTTTTTCTATAGACTTTTTTCANATAACATCTTCTGAGTCA
TAACCAGCCTGGCAGTATGATGGCCTANATGCAGAGAAAACAGCTCCTTGGTGAAT
TGATAAGTAAAGGCAGAAAAGATTATATGTCATACCTCCATTGGGGAATAAGCATA
ACCCTGAGATTCTTACTACTGATGAGAACATTATCTGCATATGCCAAAAAATTTTA
AGCAAATGAAAGCTACCAATTTAAAGTTACGGAATCTACCATTTTAAAGTTAATTG

20 CTTGTCAAGCTATAACCACAAAAATAATGAATTGATGAGAAATACAATGAAGAGGC
AATGTCCATCTCAAAATACTGCTTTTACAAAAGCAGAATAAAAGCGAAAGAAATG
AAAATGTTACACTACATTAATCCTGGAATAAAAGAAGCCGAAATAAATGAGAGATG
AGTTGGGATCAAGTGGGATTGANGANGCTGTGCTGTGT

25 Sequence ID 533

CTTGAACCTCGGAGGCAGAGGTTGCAGTGAGCCGAGATCACGCCACTGCACTCCAG
CCTCGGGGACAGAGCAAGACTCCATCTCAAAACACACACACACACACACACACACA
CACACACACACAAAACAGATATACACTGAACACAGCACAAGTGGGACATAAGAG
ATTTAAAAGGGTTAGAGATGTAAAATGGATCTAGGAATGGAAACCATAAGGNGGGA

30 TTTATCAACTGGATTCTGCANAATGCTGTTAAGGCCAGATGTTAGCAGGTGTTACA
TAAAAAAGGGATACCATGAGCAAAGTATTTGAACATGGGCAATGGTTGAAACAAG
TTTAAACAGATTATNTTTATTACCAAATCTCTCAAACCTTTAATATGCTATAAACA
TTGTGAAACAATAAAAAAACTTTCCAAAA

35 Sequence ID 534

GGGAAGGGAGCTATGAGTGTGTGTGTTGTGTATGGACTCACTCCCAGGTTCACCTG
GCCACAGGTGCACCCTTCCCACACCCTTTACATTCCCCAGAGCCAAGGGAGTTTAA

- 174 -

GTTTGCAGTTACAGGCCAGTTCTCCAGCTCTCCATCTTANAGAGACAGGTCACCTT
GCAGGCCTGCTTGCAGGAAATGAATCCAGCAGCCAACTCGAATCCCCCTAGGGCTC
AGGCACTGAGGGCCTGGGGACAGTGGAGCATATGGGTGGGAGACAGATGGAGGGTA
CCCTATTTACAACTGAGTCAGCCAAGCCACTGATGGGAATATACAGATTTAGGTGC
5   TAAACCGTTTATTTTCCACGGATGAGTCACAATCTGAAGAATCAAACTTCCATCCT
GAAAATCTATATGTTTCAAAACCACTTGCCATCCTGTTAGATTGCCAGTTCCTGGG
ACCAGGCCTCANACTGTGAAAGTA

Sequence ID 560
10   GGCGGAGGTTGCAGTGAGCTGAGATGGCGCCATTGCTCTCCCAGCCTGGGTGACAA
GAGCAAAACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAAAGCAATTTACTTAAAAAC
ATACAAACACAGAGACAAGTATTTTTGAGAAACAAATACCTTTTTCATTTTTTATA
CCAATGTAACAATAATCCATTAAACACACCTTTACTAACTGTTTTCTAGGAGTCTG
ATATGATGAGGAAATAGGTAAACCTTTAATAGCCAGTACTAAATTAGAGTGGCACA
15   ACTTTCACTGGGAAAAAGATGGGTATTTTACTTTTCTGTTTTAGAAAAGTGGCTT
GACAACAGTATGCTTATGTCTTAGAGTTTGAAATTCAAGTTCTTGAACATTATTAA
TGGCTACAATCATTCATACCCACATTGGGCTGTATTCTTGATGAATCCAAAGTGAT
TTTCACCTCAACTCTGAATTTCATTCTCCTCTTTTGAATATAATACAACCATCTCA
CTAGAGGAAGCATTTCAGTCTTTTCTGATTGGAGATTCATTATTGTTTTAGATAAT
20   GTTTTCATTTGCTTATGGGTATATAAAAATTTTATCTTAAAAATATTTCCTCTCA
TTTAGCTAGCAACATTGTTTTC

Sequence ID 561
CTCAGGGTGATCTCTGAACCCAAACTTGCCCCAAAGAAGGTTGCTCTGTCCTCTCC
25   ACATCCCCATCTCCTCCCTAGGGCCTTGTTGGGGAGAGGCTCCTCCATCTTTCCCA
AGTCACACCATCGTTTCCTACGTGGTCTGGACAAGAGCAAGAGCACACCTTGTCCC
CACCTTCTCCAGAGCAGCCAGAACCCACCTCAGGTGCCTTCCCCATCCGGTGCAGT
TAAGGCACTTCTGCCAGCACCATGGTATGAGCACTAGACTTGGAGTTAAGATTTGA
GAGCCCCTCTGTCACTGTGGAAGCTTGAGCATGTTGCTTGATCTCTCTGAACCTT
30   GTGTTTCTCATCTGTGAAAGGTGATAATGTGGGCTGCTGTGAGATTTAAAGGACA
TAATGCACCTACGGTCCAAGCACTGCCTGGAATACAGCANAAGCTCAACAGATACT
GGACAACCCATCCCCTTAGTAGAGGCACTAACCATGTGACCCAAGGCAAAAGTGCT
TAAAAAAA

35   Sequence ID - 562   nt: 580
ATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCGTTCTGGTAAAAA
GCTGGAAGATGGCCCTAAATTCTTGAAGTCTGGTGATGCTGCCATTGTTGATATGG

TTCCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGC
TTTGCTGTTCGTGATATGAGACAGACAGTTGCGGTGGGTGTCATCAAAGCACTGGA
CAAGAAGGCTGCTGGAGCTGGCAAGGTCACCAAGTCTGCCCAGAAAGCTCAGAAGG
CTAAATGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGGAAGA
ACGGTCTCAGAACTGTTTGTTTCAATTGGCCATTTAAGTTTAGTAGTAAAAGACTG
GTTAATGATAACAATGCATCGTAAAACCTTCAGAAGGAAAGGAGAATGTTTTGTGG
ACCACTTTGGTTTTCTTTTTTGCGTGTGGCAGTTTTAAGTTATTAGTTTTTAAAAT
CAGTACTTTTTAATGGAAACAACTTGACCAAAAATTTGTCACAGAATTTTGAGACC
CATTAAAAAAGTTAAATGAG

Sequence ID 563

GCAACCTGCACAACCCCGCCCTGTTCGAGGGCCGGAGCCCTGCCGTGTGGGAGCTG
GCCGAGGAGTATCTGGACATCGTGCGGGAGCACCCCTGCCCCCTGTCCTACGTCCG
GGCCCACCTCTTCAAGCTGTGGCACCACACGCTGCAGGTGCACCAGGAGCTGCGAG
AGGAGCTGGCCAAGGTGAANACCCTGGAGGGCATCGCTGCTGTGAGCCAGGAGCTG
AAGCTGCGGTGTCAGGAGGAGATATCCAGGCAGGAGGGAGCGAAGCCCACCGGCGA
CTTGCCCTTCCACTGGATCTGCCAGCCCTACATCCGGCCGGGGCCCAGGGAGGGGA
GCAAGGAGAAGGCAGGTGCGCGCAGCAAGCGGGCCCTGGAGGAAGAGGAGGGTGGC
ACGGAGGTCCTGTCCAAGAACAAGCAAAAGAAGCAGCTGAGGAACCCCCACAAGAC
CTTCGACCCCTCTCTGAACCAAAATATGCAAAGTGTGACCAGTGTGGAAACCCAAA
GGGCAACAGATGTGTGTTCAGCCTGTGCCGCGGNTTG

Sequence ID - 564   nt: 671
GGAATAGAATTTTAAATAGTAATAACTGCTTGTTTTTTTGTGCAAGTACTTTTAT
ACATAAGATAAACAAAAACCTTACCACCAAACATACCAAAATGCACCTCTTTCATA
AGTGAGTTACTAAGATTTCTATACCTGGAATATCATGTATGTTTCATTTACTGGAT
GTTTACATTTTAGGAAGGAAAATAGTTTTGTTTATTTAAACAACTGAATACTTATA
AACTGTTGTTCCTGGAAGTTATTTATTCCATAAAAAATTTGTTCTTTTGTCATGAA
TTTATAATTCCTAAATGAAGACCAGAAAGTACAAATTGCTGGGAGGAAGAATAGGC
TTTATTAATCAACTGATGTCTTGATTTTTCTAAATGGGAAGATTGCTTTATTTTTA
ACACTAATTATGGGAGCAGATTCTTAGCAAACTTCTTTGGAAAAGTTAATGTTATG
ATGTGCATTAGGCTGCCCCATCGTGTATATAAATGAAGCAGATTTGATTTTTGTAT
TCTTACGTTTCTCTGCTTTGTAGTTGTGGCTGTACTTAAAGAAATACAGAATTTCA
TATATTTAAAAATGTTTAAAATGTGACCCACAGACATTGTAAATGGATTNAAAACT
AACATGAAAAATATTCAACCTAAAAGAATTCTTAACTTCACAAGTGTTTTACTTC

Sequence ID 565

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CTTGGTTCCGCGTTCCCTGCACAAAATGCCCGGCGAAGCCACAGAAACCGTCCCTG
CTACAGAGCAGGAGTTGCCGCAGCCCCAGGCTGAGACAGGGTCTGGAACAGAATCT
GACAGTGATGAATCAGTACCAGAGCTTGAAGAACAGGATTCCACCCAGGCAACCAC
ACAACAAGCCCAGCTGGCGGCAGCAGCTGAAATCGATGAAGAACCAGTCAGTAAAG
CAAAACAGAGTCGGAGTGAAAAGAAGGCACGGAAGGCTATGTCCAAACTGGGTCTT
CGGCAGGTTACAGGAGTTACTAGAGTCACTATCCGGAAATCTAAGAATATCCTCTT
TGTCATCACAAAACCAGATGTCTACAAGAGCCCTGCTTCAGATACTTACATAGTTT
TTGGGGAAGCCAAGATCGAAGATTTATCCCAGCAAGCACAACTAGCAGCTGCTGAG
AAATTCAAAGTTCAAGGTGAAGCTGTCTCAAACATTCAAGAAAACACACAGACTCC
AACTGTACAAGAGGAGAGTGAAGAGGAAGAGGTCGATGAAACAGGTGTAGAAGTTA
AGGACATAGAATTTGGTCATTGTCACAAAGCAAATGTGTCGAGAGCA
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Sequence ID 566
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GTCACCAAGAGCTTGTTGTCAGGTTTTCACTTGCTATTCGCAGAGATTTTTTTTAA
AGGCACTATTTGTAGTGTTAAAAGGGTGAATTTATCANAAGGCATAATAATCATAA
ATGTGTATATGCCTAATAATAGAACTTTAAAAGGCATGAAGCAACACTCAAAAGGA
TTAAAGGGAGATCATCTCACCCCCTTCTTACCAATTGATAGAATGATCTGATGAAA
ACAGTAAAATAACAACAGATCTGAACACTGTCAACCATCTTGACAAATACTTATGC
CTAGTGTTCCATTATTGGAACACTAAACATGTGGAATGATTTATATCCTACTGCTC
AAGGTCATCACCAAGGTCTAATTGTAAAATTTCAAAAAATTGCAACCTCAGGCATA
AATGGGTTAATCGACATTTATAGCACACACATGCAACATGTACCAGAGATTCCTTC
TTTTCTATGAACATGGTACTTCCACCAAGATAGACCACATTGTGAACTATAAAACA
AATCTAAAAACATTTGAAATGAAGGAAATTATATAAAATATGTTCTCTTGATCTCA
ATGAAATTAAATTAATACTATAT
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Sequence ID 567
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CTCATGGCGGCCAATGTAGGCCCAAAACTTCCTCAAGTCAAACTCTCCAGGCCCAC
CTTCTGCTTCCCGGTGGCATCAACAGGCCCAGCTTTGACTTGAGAACAGCCTCTGC
AGGCCCTGCTCTTGCCTCCCAGGGGCTTTTTCCAGGCCCAGCTCTTGCCTCATGGC
AGCTGCCCCAGGCCAAATTTCTGCCTGCCTGCCAGCAGCCTCAACAGGCACAGCTC
CTCCCTCACAGTGGCCCATTTAGGCCCAACTCATGACTGTGAGGCCATTTCCAGGC
CTAGTGCCTGCCTCGTGGCTGACTCTTGAAGCCCAAAACTTCCTCAAATCAGCCTT
TTGCCCAACTTCTGTCTACTGTCGGACTCTACAGGTCAGCCTCTGCCTCACAGTGG
ACCCTCCAGACCCAGATGGTGTCTNCTGTGGCATCCTCAGGCGAAGCTCCTGCCTT
TCGGCAGCCTCTCCAGGCCCAGCTCCTCCTGCTCCAGCCTTCTCTCCAGGCTCTGA
ACTTTCTCAGGTCTCCCTCTGTTGTCCAAGGCTGGAGTGTAGTAG
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Sequence ID 568

TATATATGTAATGCCCTTAACCTAGTGTTTGGCATGATCGTTGCTGAAAGGGAAGC
TTGTGGGTACAGTGTCCCCTCAGAAGCCAAAGCCCAGGGAAGGTCGCCTGCCCAGG
TCAGGCTCCCAGCGAGTTTGTCTGGGGAGGGGCCATTCATACCTCCAGGTCAGGAC
AGAGGCTCGGGCTGAGGGAACCCTACACAGGTCCTGGAAGCAGATCCTTCCTGCCT
AAGCCAGCAGGACAGCTCAACAGGAAGCATCTTCCAGCCACGGGAGGAGAGGCAGC
ACCTTTTTGGAACCATACAGAGCTAAGAATGGTGGTACAAGTAATAGATTCTGTA
CTGGCAACCCCACTTGGTGGAGCAAGTTCTAGGAAAAGGGGGCTGTCCTTGAGTCA
GCCATGGGGTCAGCCACACAGTCACCGCAGCTGCTCTTTGGCACCGGGCGCTGGAA
AGACCTAGGATGACACAGCCTGGAAAGAGCTTGGGAAAAGCTCATCTTCCACAGAA
CTACCTGCTATACCAGCCAGGGCAGGTGCTTATTCCCACAACAGCCCTCTGTTGTA
GGCGGCAGTGCCATCCTGAANGTGCCGTGGTACCTTCTGAANACCCAGCTGAGGGC
CTGTAATGGCACTTGCATGCCACATGGNACACCCTTTCCCGGTTAA

Sequence ID 570

ACCGCGGCCGCGTNAANAAAAAAAAAAAAAAGAATTCCACTTGATCAACTTAATTCC
TTNTCTTTATCTTCCCTCCCTCACTTCCCTTTTCTCCCACCCTCTTTTCCAAGCTG
TTTCGCTTTGCAATATATTACTGGTAATGAGTTGCAGGATAATGCAGTCATAACTT
GTTTTCTCCTAAGTATTTGAGTTCAAAACTCCTGTATCTAAAGAAATACGGTTGGG
GTCATTAATAAAGAAAATCTTTCTATCTTAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

Sequence ID - 571   nt: 457

TTAGAGAGGTGAGGATCTGGTATTTCCTGGACTAAATTCCCCTTGGGGAAGACGAA
GGGATGCTGCAGTTCCAAAAGAGAAGGACTCTTCCAGAGTCATCTACCTGAGTCCC
AAAGCTCCCTGTCCTGAAAGCCACAGACAATATGGTCCCAAATGACTGACTGCACC
TTCTGTGCCTCAGCCGTTCTTGACATCAAGAATCTTCTGTTCCACATCCACACAGC
CAATACAATTAGTCAAACCACTGTTATTAACAGATGTAGCAACATGAGAAACGCTT
ATGTTACAGGTTACATGAGAGCAATCATGTAAGTCTATATGACTTCAGAAATGTTA
AAATAGACTAACCTCTAACAACAAATTAAAAGTGATTGTTTCAAGGTGATGCAATT
ATTGATGACCTATTTTATTTTTCTATAATGATCATATATTACCTTTGTAATAAAAC
ATTTTTCCC

Sequence ID 572

CGTCTATTTGNGTTTCTTCTCACAATTGGTAAGTTCTCTGTATTGATTGATGGCTA

AGTTTGATTAGTGTTTTTCTCTAGTTGGTAATTATATTCTAGTATTTTATCATCTT
ATTGTTTACTCAACTNAAAGTGNCACAGAAGAGTTGCCAGGTTTCTCTTTGATATG
AGATCTCTNNTTGATTTGGAATGCAAATCANAAGTGTCATGTTTTGAATAAAGGGA
CCAGATGACTTATAGGTATTCTTTCTCTAAATATAACTAAGGTAAGATTTTTGTTT
TGAGGTACTTAATCTATATAAGTGGTAAAGAATTTACTTGAATTTCTCCAAATTCT
CATGTCTAAAGTCTGATTGATTAAATTCATTCTTGGTATTTCATTTTGAAAAGAAT
GTAGCTTTAGCAAACCTCTTTGTATAAATGCAGTGGGATTAAGGTCATTTAAAAAA
TTGTTATATCATTGTATTTTTAAAATTTACCAGTTTTATTTTTCTTTTTACCCTTT
AGCCCGGCCTCAGAAGTGTGTTTGTGTCCATTTCTCCCAGCGCACCCTCTGCATA
TCTCTACCCACTTGTCATAATTCAGCATCCAGCAGAGGAAAACAAAGTGTTGCGTA
CAGTTCCTCTACTAGCAGCATGCCTCCCCCAGGACAAGTGTA

Sequence ID 574

TTATTGCTGACATAAAAATGGTGCACATCGGCCAGGGCCCAGGATGAATCAGCCAA
TCTGCACCATTTATACATGGAACTGGAGAACATTGTGCCAATAATCATTTAATATA
TGCCAAATCTTACACGTCTACTCTAAACTGCTCTAATGAAGTTTCAGTGACCTTGA
GGGCTAAAGATTGTTCTTCTGGGTAAGAGCTCTTGGGCTGGTTTTTCANAGCAGAG
TTCTTGTTGTGGGTAGACTGTGACTAGGTTCACAGCCTTTGTGGAACATTCCGTAT
AACGGCATTGTGGAAGCAATAACTAGTTCCTATGAAAGAACCAGAGCTGGGAAGAT
GGCTGGGAAGCCAGGCCAAAGTGGGGGCAACAGCTTGCTTCTCTTTCTCTTCTCAC
CCTCAGTTTGTATGGGAAAATGGAGATGTCCTCTCCACTTTATCCCACGATATCTA
AATG

Sequence ID - 575   nt: 209
CAGGATATCGAGACCATCCCAGACAGCATGGTGAAACTCCGTCTCTACTGGAATAC
AAAAAGTTAGCCGTGTGTGGTGGCACGCGCCTCTAATCCCAGCTATTCGGGAGGCT
TAGGCAGGAGAATTACTTGAACCCGGGAGGCGAAGGTTGCAGTGAGCTGAGATCGC
ACCATTGCACTCCACCCTGG-CGACAGAGCAAGACTCCGTCT

Sequence ID - 576   nt: 541
CAGCCAACCCAGAAGGAGCCAGTCTACAACTATGCCTGATCCTCCTCATGGCAGGC
CACGAAGCATTGCTGCCATGTGTTGAATTATAAAACCCACATTGCTTTTTGAACCC
TGTTGCGGGTAAAAATAACCAAATTATCAGTCCTTGGAAACCCAGGCAATCAAGTG
AGTACAAGGTAAAGATAAGTATGGTTTAGAGGAGAAATTATGTTCCTGAACTGGTG
TCCTTTGATGGCAGCGTCAGCCTTGCTAAGTCAGAGTAGAGGGAGCAGTGACCTTA
ATAAGCTTTGGTGAGCATCATGTGCACGCGTGGGTGGGAGTCCCTTTCACTGATGC
TTTTAAAAGTGCTTTTGCAGACCCTGGAAGGGATCCTCCACACATATGAGGTGTGG

- 179 -

GACAGGTAGGCCAGAGAGGATTAGCCCTGCTTTCGAGACTAGAAATCTACAGTCCT
GAAGGAGCAGTAATTAATTGGTACACCTGTCAGGGCCAGCCCCCAGGTCTCCTGGC
TTTTTCCAGGTTTTCTGTCTCACATGATTTTGCTTTT

Sequence ID 577

CTTTAATTTTTCAAGTGTTTAAAAAACAATTTTATACTTAAGCCAGCCTTGAAGAT
AAGCACAAAATTTACCAGTTTACATTTAAAAAACAAACAAAAAACGACAACAACTC
AAGCACCCGCTCTGTGCATAGCACTATTCTAGGTGCAATAAAAGGGAATCTTAACC
TTAGAAATATGAGTTCACTTTCTGGAATTGTATTATCTCCTTTTCCAGAGAGTAAA
AATAAATAAAATCACCATTGTTTACTACAGATCTGCCCCAAACCACATCTGGTTCA
CAGAAAGGCTAATTTCTGCCAAATTAAAGATGTAATGAACTCAGTTCCTGCTTTCC
CAAAAACACGAAAGCAGAATTCCTTTTCACTGAAAAAAATAAACAGTTTTCCATGC
AAGGGCAGTTTGCTTCTAATAAGTATTTTTTAAAAAATTTTTTTTTCCTCTAGCTT
TTCTTTAAATTTTCTTCCTCTAATATTGCCTTTTCTTGTACAAGGCAGACCAGGTA
TCTTTTTATGCTGTTTTTCCTTTACTAAGAAAGTATTGCATCTTGAAGACAAACC
ATTTCCCAGAGTAGTGATAAAAAATAACACTAAAAAAACTTTAAAGGTGAGTCACT
TCATCACCTTGATGAAGTAAAAAA

Sequence ID 578

GGAAAAAATATTTCCACTTAGATATTTTACATGGTTTTGTTTAAAATTACCATTAC
TTGTTTTTTAAAAACACATGACCACATATGTATATGTATATCTACCTAAACATTGT
ATCATGGTTTCAGTATGTTATTCATGTATTACTGGGAGATGCTACCAAGAAACCAA
CCCAAAGAAAATTCTGGAAAATACATTTCTATTTATAGAATAAATGTTTCATTTAT
ATAAAGCAAAAGAACTTAGAGTTCTAATAAATGGGATGTCTAATAAATTATGAAG
TTACTGATTTGAATATATTATATTTTTATAACTTCCTTGCCAAAGTCCTGATTTAG
TACATTAGAGAACCTGTGTTTCCTCTCTCCTCTACCATTCATCTCTCTTCCATACA
GTCATTTGGGCTTTTTACTCAAAGAGAATCAAGAAATAATAAGGTATAACAAGCTT
GGCAAAGTGTTGGCTTTTTAAAAAAAAATTTTTTTAATCTCTAGCAGTTTGGTAAT
TTAGCAGCATCATTTATTTGGGATTCTTTTATCTGATTTCAACAGTGAAAAACATC
CCTATGATAAAGCCTAATGACCCATTTCCAAAAGATGGAATTGCCCTTCCTAGAAA
ATATGACGGAGAAAGT

Sequence ID - 579   nt: 502

CGAATAGCCAAGTGGTCTGACAAGATCGAGAGTAATGAGGCCCATACTTTAGTACA
GTCTTGAATGGCCAGATGGTGCTGGGCATACCCCAACCAGAGATATGTAAGTCTTT
ATGTTGTCAAAATTTCCCAGAAACATGAATTTCCCACTAAGATTCATTAAGGAAAA
CTAGAATGAAAACAAAAACGTTCCTTGTATAATATTCATTANAAAGAAATGAAGAA

- 180 -

GGCCGGGCATGGTGGCTCACGCCTGTAATCCCAGCACTTTGAGAGGCCAAGGTAGG
CAGATCATGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAATCCCGTC
TCTACCAAAAATACAAAAAAATTAGCCGGGCATGGTGGCACACACCTGTCATCCCA
GCTACTCAGGAGGCTGAGGCAGGAGAATTGCTTGAACCTGGGAGGTGGAGGTTGCA
5   GTGAGCTGAGATTGCACCACTGTACTACAGCCTAGGTGACAGTGCAAGACTCTG

Sequence ID - 580   nt: 316
CCTATGCCAAACTAAAGAAAGCTTGCCTGGCCTACAGGCCTAAAGGTTCAAATGNG
GATTAAAAAAACACAGTAGTCACATAAAATGTCTGCTGGCTGGCTGGAATTCCATC
10   ACCTACAATTTACCTGCTTTCAAAAACTGTGTTCAACATTGAGAAAACAGAAAACC
ACTTATCTTGAGCTTAATATGGGCTTCTTTTTCCTTAACTGTAGAACACTTACTGA
AATATCAAATCAATGGTTAGGATATGTATCCTAGGCAGGCCTAAACCATTAACACT
TGGTTTAAGCAACTTTGTATAATTNACCTCCTAAAT

15   Sequence ID 581
CTTCATGAGTGCCCGGTTGCCCAAGTCAAAAACCTGGGAGTGATATAAACTCCCCA
CACATCCAGTCAGTCACTCATCAACTCTATTGATTCTG-CTGCTAAATATATCTCA
ATTGTATTAACTTAAACATATGCATAATACATCTTCTTCTTCACTGCATTTTTGTG
GGCTGCACTTACCTTTCAGGTAACAACAACACTGGCCCCTCTTGCCCTTCTAGTCA
20   GAAGTGCCAAAATGATGAGAGCTAGCCATGACAAACCCACAGCCAACATTACACTG
AATGTGCAAAACTGGAAGGGCATCCAAACAGAGGAGG

Sequence ID 582
TAGAATTCTCGCCTGCCTTGGCTTCTCCCTCTAGTTGTTCCTTCTCTGTCTTCTGT
25   GGGCTTCTTATTGTCTGCTCACTCCTTCTTCAGTGTCCTCTCATGGGCTTCCTTCC
CTTCTCAGCTGATGCCATCACCTGGGGAATCACAGTTACTCAGCAGCACTGGGGCC
TCTCTATCTCTATGCTGGTCATGCCTATGTGTGAGCTGCAGACCCAGTGGAATTTC
CATTTGTGCATCCCATGCCCAGCCCACCCTCCACCAGCCTCGAATGCAGCTGTTCA
GCCCTACCCCAGTCCTCAGAAAAGTTCCTCTCCCTGGATCCTCTTTTTCCTTCATG
30   AGTGCCCGGTTGCCCAAGTCAAAAACCTGGGAGTGATATAAACTCCCCACACATCC
AGTCAGTCACTCATCAACTCTATTGATTCTGTCTGCTAAATATATCTCAATTGTAT
TAACTTAAACATATGCATAATACATCTTCTTCTTCACTGCATTTTTGTGGGCTGCA
CTTACCTTTCAGGTAACAACAACACTGGCCCCTCTTGCCCTTCTAGTCAGAAGTGC
CAAAATGATGAGAGCTAGCCATGACAAACCCACAGCCAACATTACACTGAATGTGC
35   AAAACTGGAAGGGCATCCAAACAGAGGA

Sequence ID - 583   nt: 631

CTGAGGTGGGAGGATTCCACTCTCACCCATTTCTTCTTTCATTTTCAGTTTCTCCA
GTTAGTAACTGAAGATGTTCTTTGAGTAATTAAGTGAGTGAGAAAATTTTTAAGTG
AGAAATCTATAAAAAGAACCATGTTAACATAAATATTTCAGTCCTTACAAGTTGGT
ATTGACTTTTCTCATTGGTAATCTGACTGATTTAATACTGCTCATTCCAATATCTG
GTGATGTAATTCTGGTTATGAATCCTTGTATTAATAACACCTCCTGGGAGGTTTTT
TTTCCCCAACATTACATTCAGAATATTAGAGCTGAAAATACCTTTTTTAAGGTTAT
CAGGAGGAGGGAGCTTATGTTTAATGTGGTGGATAAAACTTAACTGCTGGTTAATA
CAATTGTTATTCAGGTGAAATTCCCTAAACTTTTCACGTGCAAAGTTTTGTATGTA
TACAGACATTTGGGGAAAGTTTTATCATCCCTAAAACCGGTTACTGTCCAGAAAA
TGATAAGAATCCCTGGGTTCCAAATCCTTCATAAGGTATTTATTCATTTATTTATT
CAACACATTTACTCAATGCCTCCGCTCTGCTGCAACTACACTGACATTCTGCTTCT
AATCTAACCGAAAAT

Sequence ID 585

TTTCAAATTGTACAATAACACAAACAACTTTGTTAAGGCCATGTTTTATTTGCTGA
TTAATGGACAAAAGGCAATGTAATTTATTTTCAAGTATTTTCTTGAAAGTCTGTGC
TCATAAAAATCATGAAAAGTTGGAAAGACTGTTAAATCACTGAAACTTCAAATATA
TCTTACACAATCTTGTTTGTACAAAAATACAAGTTAAATATAAACATAAAGCAATC
ATGGTAATTTTATGCAAATCTGTTTTATGTGATCATCAGTTATATATAAAAGTTTC
TCAGTTCTGTTATTTGTGAAAGATCAATACCAGATTGAATGACTACCTATTGGCA
AAGGGCCCTAAAAAGCTTACTTTAGCACTCATCTTTTACATGGTTAAATGCATTTC
CTAATTTGAGATCACCTAAACACTGGAAAAGAAAAAAAATGAAAGGGCAGTATGTC
CATAAACCAACAAATAATTTGGCTGTAATGTATCATAAAACACAAACCCCACACAT
CTGTACAATAAACATTATGTATTACATACACACAACACACACCCAGTCATAAAGCC
TAATGATGTGCTGCTTCCAGTTCAATATTCAGCTGTGCATTTTTTCTTATTTCATC
AAATGAATAGCTTTTTGTCACC

Sequence ID 586

GTAAACTGTTCTCTCCGAGGGAAAAAATGGAAGTTATCCTCACAGTTCACTGCCGT
GGTATTTCTTCTGTCCCATGCTTTGCATGACTGCCATGGTACAGCCTTGTTTCAAA
CTGTTCACTGTGATCTGTGGGTCTTTGAGTTTCAGTGAGTTTGCTGAAATGTCGAA
GAAGTAGTTCCAAACTTCAATGTTCAATGAAATTTTTGTTCAAGTTTGAAATGGAG
AGAGCAGCTTTAAAAGGTACTAAGCCTTTTACAAATTGGTGAGTACTGGCACATGA
GAT

Sequence ID 587

TTTTTTTTTTTCCTTAAAAGGTAACCCCTAAACACAGCTAAAACTATGCCATCAGC - - - - - - - -

- 182 -

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TGACTCCAAGGNACACACAGTCCTGTATCTGGAACTACTGAGTGGCAGGCATCTTT
CTCTGCCTCTGACAGTGGAGTCCCCATCACTGCAGAGCATAGCCAAAGGAGTCAAA
GGTCTCAGCGGGTCACTGCCTTATCAACCCTCACCAGTCCCTTATGTTTTTTAATA
TTTTATAATCTTGACATGACACCAAGATGCTTTAATAAAAAAGCACCTCTAACTCG
GTCTTGTATTCACTTACCTTGAGCCTGGGACTTCTCTAGGCTCCTGAGGCAAAAAC
AGGTAGAGGGGAGATGGTGGAACATAAAACACAATTTTGCTTGGCACCCACCTTGG
CGTCTGTCCCCATGACCAGGTCTTTCAATTCGATGATTTTGTCATTGATGGAGGAG
CGATATCGTTTCTCAATGATATTATGGGTTGTCCGCCTTTCTCCTTCTTTGGGGGG
CTCAAGCTGCTTGACTCCCCCAGGTACCTGCTTAATGGGCACTTTCTCTTGCCCC
ATCATTACAGGCATTGTGGTCAGAATGGTCCCACTGCTGCCCACCAGGGTCTA
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Sequence ID 588
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CTAGTCTTTTCATAGTCTGCATAGAGTCTGGCCATTACCATCAGTTTTTAAGATGT
CCATATTGTGGCCGGGCGCGGTGGCTCACGCCTGGTAGTCCCAGCACTTTGGGAGG
CTGAGGCAGGTGGATCATGAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTG
AAACCCGTCTCTACTAAAAAAAATATTAAAAAATTGGCCAGGCCTGGTGGTGGGCG
CCTGTGGTCCCGGCTGCTTGGGAGGCTGAGGCAGGANAATGGTGTGAACCCGGAAG
TCGGAGGTTGCAGTGAGCCAAGATTGCACCTGGGCAACACAGCGAGACTCCGTCTC
AAAAAAAAAAAAAA
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Sequence ID 589
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CAATTATTTATTACCTTTCCATTTGTTCGCCTGATGATGTGACAATGCATGGTCTT
TGTGCATGCTGCTAGACACTTTTCTTTCCCAGCCGAAAAGTCTATTATGTAATTTT
TACATTCATAATTTTAATGTGGATGATCAGGATTAAATCAAGATATATATCTGGAA
CCTCTTATAAATGGAGCACTTAGAAATTTGTTGTTCTGCACTTAACCTAGAGAGAG
AAAAAATGCTTTTCTTTGTGAAAAATCTGAATTCCTGTCCTGACCTTCTGTGATGT
GGAAACCCTAGGCTCTGAGACACACTCTCTGGTGTCTGAGACAGAACCAAAGCAAT
AACGTTGTGATGCCCACAGGCCTGGAGCCAGCTAGCGACCTTGTGCCGCCCAGCTG
TCCATGGCCCGTGCAGAGCAGAGGACAGTGAGTGTCTGCACTGAGAACCTTAAACC
ACAGTTGAACATACCCACACCTGTTTGTCTTAAGCTATAGTGTAAAAACAAAGTTT
GGGCTCTGAAAATTTAACTGAAAAGATTTCCTTGTT
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Sequence ID 590
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GTGGCAGCAGGCGCAGCCCAGCCTCGAAATGCAGAACGACGCCGGCGAGTTCGTGG
ACCTGTACGTGCCGCGGAAATGCTCCGCTAGCAATCGCATCATCGGTGCCAAGGAC
CACGCATCCATCCAGATGAACGTGGCCGAGGTTGACAAGGTCACAGGCAGGTTTAA
TGGCCAGTTTAAAACTTATGCTATCTGCGGGGCCATTCGTAGGATGGGTGAGTCAG
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- 183 -

ATGATTCCATTCTCCGATTGGCCAAGGCCGATGGCATCGTCTCAAAGAACTTTTGA
CTGGAGAGAATCACAGATGTGGAATATTTGTCATAAATAAATAATGAAAACCTAAA

Sequence ID 591

CAGCAGCAGAAATGTTTGCAAGATAGGCCAAAATGAGTACAAAAGGTCTGTCTTCC
ATCAGACCCAGTGATGCTGCGACTCACACGCTTCAATTCAAGACCTGACCGCTAGT
AGGGAGGTTTATTCANATCGCTGGCAGCCTCGGCTGAGCAGATGCACAGAGGGGAT
CACTGTGCAGTGGGACCACCCTCACTGGCCTTCTGCAGCAGGGTTCTGGGATGTTT
TCAGTGGTCAAAATACTCTGTTTAGAGCAAGGGCTCAGAAAACAGAAATACTGTCA
TGGAGGTGCTGAACACAGGGAAGGTCTGGTACATATTGGAAATTATGAGCAGAACA
AATACTCAACTAAATGCACAAGTATAAAGTGTAGCCATGT

Sequence ID 592

TACTCAATGAAAAACCATGATAATTCTTTGTATATAAAATAAACATTTGAAAAAAA
AAAAAAA

Sequence ID - 593   nt: 565

CAGGATCAAGGTGAAAAGGAGAACCCCATGCGGGAACTTCGCATCCGCAAACTCTG
TCTCAACATCTGTGTTGGGGAGAGTGGAGACAGACTGACGCGAGCAGCCAAGGTGT
TGGAGCAGCTCACAGGGCAGACCCCTGTGTTTTCCAAAGCTAGATACACTGTCAGA
TCCTTTGGCATCCGGAGAAATGAAAAGATTGCTGTCCACTGCACAGTTCGAGGGGC
CAAGGCAGAAGAAATCTTGGAGAAGGGTCTAAAGGTGCGGGAGTATGAGTTAAGAA
AAAACAACTTCTCAGATACTGGAAACTTTGGTTTTGGGATCCAGGAACACATCGAT
CTGGGTATCAAATATGACCCAAGCATTGGTATCTACGGCCTGGACTTCTATGTGGT
GCTGGGTAGGCCAGGTTTCAGCATCGCAGACAAGAAGCGCAGGACAGGCTGCATTG
GGGCCAAACACAGAATCAGCAAAGAGGAGGCCATGCGCTGGTTCCAGCAGAAGTAT
GATGGGATCATCCTTCCTGGCAAATAAATTCCCGTTTCTATCCAAAGAGCAATAA
AAAGT

Sequence ID 594

CAGAAGAGTAAGCAAATCTCAAAGCAGCGAAAGGGAAGAAACTAAAAAAGGTAGAG
CAGAAATAAGAGAAAATAGAGAAGAGAACAATTGAGAAAAATAATTGAAACCAAAA
GGTGGTTCTTTGAAAAGCCTAACAAAATGGACACATCTTTAGTTAGAGTGACCAAG
AAAAAAGGGCAGTGACTCAGATTACTTCATTCAAGAGTGAAAGAGGGCACATCACT
ACCAATTTACAGAAATAAAAAGGATTATGAGGAAATACTACAGATAATTGATGACA
TTAACTTAGAAGAATATATTTCAAGAAAGACACAAACTACTGAAACCGACTCAAGA
AGAAACAGAAAATCTGAACAGACCTATAAAAAATAGAGATTTAATTGATATTCAGA

- 184 -

AAGTTTCCCAAAAAGAAAAGCACTGGCCAAGATGACTTCACTGGTGAATTCTATCA
AGTGTCAAAGATGAATTACTGACATTCATTCACACTCCTTTAAGAAATAGAAGAGG
GGACATCACTTTTCAAAGCATCGACATTCTAATCATTAGTCCCTTGGTTTCCTGCT
CCCAAAGCCAGGTGATGTATCACAAAAAAACCCCTACAGACCCACTGGGCACAATG
5   GCTTTATGCCTAT

Sequence ID - 595   nt: 98
CTTTGCTCGAATNGTCAGATAAGGATTCTGTGAANGGAGATGAGATTTCCATCCAT
GCTGACTTTGANAATACATGTTCCCGAATTGGGGNCCCCAAA

10

Sequence ID 596
CTCAAGTGTTCCCTCAGCTTAGGCTTTGTTTAAATGATCCCACCCAGGGGCGATGG
TAGGGAACAACAGGGTCACTAAACTATTTGGCTGGCTACAACTCTGGGAAATGGTA
AGACAGGGAAAGGCCATGTTGTTCATTCCCTTGTGCAGATCTAGGGAGAACCGCAG
15   AGAGAACAGTTAGCATTTCTTGTTCAATGAATTATCCTATTAAGAACACTGGATGT

Sequence ID 597
CGGNCGCGGTCGACGCTACTCCTACCTATCTCCCCTTTTATACTAATAATCTTATA
AAAAAAAAAAAAANAAAAAAAAAA

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Sequence ID - 598   nt: 362
GGCATGTGCCTGTAGTCCTAGTTGCTGAGGTAAGAGGATTGCTTGAGCCCAAGAGT
TCAAGGCTGCAACAAGCTTTGATTGCGCCACTGCACTCCANCCTTGGCGACAGACT
AAAACGCTGTCTCAAAAAAAAAACAAAACGACNAAAAAAAAACAAAACAGAAAAA
25   ATTAACTTAGGCAATGACAGTCCCTGGCAAATGCTGGGAGGGAGGCAACANTGGTC
AAGGAAGGTAACCCTGAANCAGGACTTGTAAAGCAAATAANATTGGGAGGCCAAGG
TGGGTGGATCACNAGGTCAGGAGTTCGAGACCAACCTGGCCAACATAGTGAAACCC
CGTCTTTCTAAAAATACAAAAAATT

30   Sequence ID 599
GACAAAAGAACCATTTGGATACATAGGTATGGTCTGAGCTATGATATCAATTGGCT
TCCTAGGGTTTATCGTGTGAGCACACCATATATTTACAGTAGGAATAGACGTAGAC
ACACGAGCATATTTCACCTCCGCTACCATAATCATCGCTATCCCCACCGGCGTCAA
AGTATTTAGCTGACTCGCCACACTCCACGGAAGCAATATGAAATGATCTGCTGCAG
35   TGCTCTGAGCCCTAGGATTCATCTTTCTTTTCACCGTAGGTGGCCTGACTGGCATT
GTATTAGCAAACTCATCACTAGACATCGTACTACACGACACGTACTACGTTGTAGC
TCACTTCCACTATGTCCTATCAATAGGAGCTGTATTTGCCATCATAGGAGGCTTCA

TTCACTGATTTCCCCTATTCTCAGGCTACACCCTAGACCAAACCTACGCCAAAATC
CATTTCACTATCATATTCATCGGCGTAAATCTAACTTTCTTCCCACAACACTTTCT
CGGCCTGTCCGGAATGCCCCGACGTTACTCGGACTACCCCGATGCATACACCACAT
GAAACATCCTATCATCTGGAG

Sequence ID - 600   nt: 595
TTCAAATTCTTGNTAANAGTCTTTGTTCTGAATTTTACTTTGTCTGTTATTCCTAT
AGCCTTTCCAATTTTCTTTCGCTTGGATTTTACGTGATAAGTTTTTTCCCCCATTT
TACTTTTANCAACTCTATATTTTTAGTTGAGGTTGGGTTTCTTGTAAACAGCATA
TAATTTGGGTTTTTAATCCAATCTGAAAATTAATGTCCTTAATTTTGTGTTTATA
CCATTTACACATAATGTACTCATATATAAGGTTTAACTGAAACCTACTATCTTGCT
AGTTGTGCTCTACTTGAATTTTTTTTTAGTATTCTGTTTTAATTGACCAACATTTG
ACTGTATCTCTTTGTGTAATTCTTTTACAGGTTGCTGTAGGCATGACAATATATAC
ACTTAACTTTTCTCAGTACACTGAGAGTTGAAATTGTAGTACTTCGAGGAAAACAT
AGAAAACTTGCAATGATATCGGTTACATTTTACCACCTCCATATGTTGCAATTATT
AAATGTATTAGATCTGCCTACCTCGAAAACCCATCAGTCTTTTAACTTTGCTCTCA
ATGGTGATTCATATTTTTAAAAAAACTTGAGGCAA

Sequence ID - 601   nt: 522
TCGACCGGGTTTGGAGCAGTGCCTTGTTTGCTGTGCAGCGGATACTCTACAGGTAC
ATTTCCTTTTTGGAACCAAAAGGGAGGGATTTGACAATATTGATGGTAGATCTTTT
TTCTTTAGCAAGAATTAAGGATTTTGGTGGGTGGGGGGAGGCTTCTGTGGGGACCA
AGACAATGTACTGTCAGTCAGGATTTAAGTCGAACTACCTCATCCCTTGCCCCAGA
GAACAGTTGATCGTGTTTTAAACCAAAAGGTGCGGAATGGAGAGAGGGAGGCGGTG
CATTGCAGCTTCCGATAGAGCTTTTTATTTTTGGATATCAGGAACCAATTTTGAAG
ATTTCTTAAGAAAGTCATTTACATCAGGGACATGAAGAGCAAAGTAGGTATTTTTG
GTCAGTACTTGAATTTGATAGGCTTTATGCAAACAACTCTCCCTCTGCTGGAGTCT
GGCAAGTTTGCTTTTCACTGGACGCTAATTCAAGTGCCATACAAAACTAAAATAAN
AGTTTTACTTATAACACA

Sequence ID 602
CAGAAATCGCAATTGAAGACCAGATTTGTCAAGGTTTGAAACTGACATTTGATACT
ACCTTCTCACCAAACACAGGAAAGAAAGTGGTAAAATCAAGTCTTCTTACAAGAG
GGAGTGTATAAACCTTGGTTGTGATGTTGACTTTGATTTTGCTGGACCTGCAATCC
ATGGTTCAGCTGTCTTTGGTTATGAGGGCTGGCTTGCTGGCTACCAGATGACCTTT
GACAGTGCCAAATCAAAGCTGACAAGGAATAACTTTGCAGTGGGCTACAGGACTGG
GGACTTCCAGCTACACACTAATGTCAATGATGGGACAGAATTTGGAGGATCAATTT

ATCAGAAAGTTTGTGAAGATCTTGACACTTCAGTAAACCTTGCTTGGACATCAGGT
ACCAACTGCACTCGTTTTGGCATTGCAGCTAAATATCAGTTGGATCCCACTGCTTC
CATTTCTGCAAAAGTCAACAACTCTAGCTTAATTGGAGTAGGCTATACTCAGACTC
TGAGGCCTGGTGTGAAGCTTACACTCTCTGCTCTGGTAGATGGGAAGAGCATTAAT
GCTGGAGGCCACAAGGTTGGGCTCG

Sequence ID - 603   nt: 624
GACACACGAGCATATTTCACCTCCGCTACCATAATCATCGCTATCCCCACCGGCGT
CAAAGTATTTAGCTGACTCGCCACACTCCACGGAAGCAATATGAAATGATCTGCTG
CAGTGCTCTGAGCCCTAGGATTCATCTTTCTTTTCACCGTAGGTGGCCTGACTGGC
ATTGTATTAGCAAACTCATCACTAGACATCGTACTACACGACACGTACTACGTTGT
AGCCCACTTCCACTATGTCCTATCAATAGGAGCTGTATTTGCCATCATAGGAGGCT
TCATTCACTGATTTCCCCTATTCTCAGGCTACACCCTAGACCAAACCTACGCCAAA
ATCCATTTCACTATCATATTCATCGGCGTAAATCTAACTTTCTTCCCACAACACTT
TCTCGGCCTATCCGGAATGCCCCGACGTTACTCGGACTACCCCGATGCATACACCA
CATGAAACATCCTATCATCTGTAGGCTCATTCATTTCTCTAACAGCAGTAATATTA
ATAATTTTCATGATTTGAGAAGCCTTCGCTTCGAAGCGAAAAGTCCTAATAGTAGA
AGAACCCTCCATAAACCTGGAGTGACTATATGGATGCCCCCCACCCTACCACACAT
TCGAAGAA

Sequence ID - 605   nt: 338
ACCTGAGGCCTCGGTGGGGCCAGTGCGACGCTGGCTTAAGGAGCTGGAGGGGGTTCC
TAATACACATTTAATTCAGTTTCTCTTCCCTAAGAGGCTGCCGGAGTTGGGGCCTC
CTCCAGCAGAGACCCTCGGACCCCTGCAGGGCCTGGACTTGGGGTGAACAGGGCTT
CAGTCAGCGCAAGTATTCCATTTGCATTTGGTAATTTTTCATGCCACCTATTTATG
AATATATAAATCTTTATACCAAATCTATTTTTTAAAACATGGAAAAGTTGCCTTTA
TGGAAACTTGGCAGAGCCAGAGTGTACACATTCCTAAACCATTAAACAGATTTCTA
TA

Sequence ID - 606   nt: 556
GGATAATGATACCTCTGACCTTTCTTCCTTTTGGGAAGTACTTGAGTGTGCAGCTG
CATGAGGCCTCAGCAGGAGAGAGATTTTAGGTCCAAGAAGCTATACCAGTAGGACA
AGGCAGGAAAATACTACACTTTCAGGATCAAGCCCCTCTGACTCTCATTTGGAAAC
TGGATGTTTGCTAAGCACCTGCTTCTTAAGGATGCCGAGGGATTTAATGATACTCC
CAGAAACCTGGAGAGATTAATGGGGCCTATGGAGAAGTGCTCTGAACTCAGTGTTG
GGACTTGAATAAAATTAACCATTGTCATGTTTTCAGAACAACTAAGCTGTTTTATA
TTTCATGTGCATGAAAGCCCTAGAACTAAGTTGTGTTATTTCCAGAAATGAAATAG

- 187 -

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ATCCCACAGTTAGATGATGTGGCCATTAGGAAGTACCAAATTTATAAAAATCACTG
GAGGTCTGTCTGAGCAGTACCTAATAAAATATAGTATACTGAAAGTGAACAGATCT
TTGTCTCTTTCTTTGGCTGCTTGATACTTTATCTGTGTCTGCCGGACAGTGC
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5   Sequence ID 607
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CAATAAAAGCAGGTTAACCTCAATGATAGCAGTTAAAATGTTCTATCTTATGTATT
TCTTTTAAGTATTACCATTATGGTGCTACTGAGCGTTTTCTTTTGGTAAAAAGAAA
AATGCCATGGGCTGCAGTCTTCTTCCATCACTTTTCCCTACCAGGTCCATTAATAT
GCTTATAACACTAGTGCCAGTTATTTTATTTGATAATGCTTATGGTATTTGTATAT
10     TTGTTTGCATTCCAATTTTGTTTAATAATGAGTGTGTAAACTGCATACGTTAAATA
AATGTAAATACTAATGTACTGCTGC
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Sequence ID 609
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TTTTATTACCCAAGTTTTAACCTCTGTCTGGTGATTTGTTGTTGTTGTTGTTGTNG
15     TTGTTGTTGAAGTTCAGGCTGCATGTGGGATAGGTTTGCTCAGGCATACTTCTTAG
GAAGTAGTCACTTGCATGACTGTTTTGGGATAACTCTTTGAGTATTTGGAGAGGT
CTATTGTAACTTCTGAAAGGCATTGTTTTTACGTATGAATGTTCTAAAATTCATTC
TAAATGGTCATGAAAAGAAAGGATTCACATTTTAGAATGGCAATAGTCCCTGAGG
ACTATTATGTCTTTTAGATTTCCTGTGGGTTTCTAGGAATGTTAGTGTAACTTANA
20     TTTCCACCTACCTGATTTCTGGATGTGCCTATTGGAACTTGCTGAGATCTTTTTTT
TTCCTTAACATGTTGTCCCCTTGACCCGTACTTCGAAACTAAACATATTATTTTAT
TTGCTTACACTTCAGGAGGCAATTGGCAGACACCAGGCCAACAGTCT
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Sequence ID 610
25
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GCTCTGACCCCAGTTGGAAATGTATCTGTACTTTGTCCGGCTTCCACTCAAGGACC
ATTTATGACATTGCTTGGTGTCAGCTGACAGGGGCTCTGGCCACAGCTTGTGGGGA
TGACGCGATCCGCGTGTTTCAGGAGGATCCCAACTCGGATCCACAGCAGCCCACCT
TCTCCCTGACAGCCCACTTGCATCAGGCCCATTCCCAGGATGTCAACTGTGTGGCC
TGGAACCCCAAGGAGCCAGGGCTACTGGCCTCCTGCAGTGATGATGGGGAGGTGGC
30     CTTCTGGAAGTATCAGCGGCCTGAAGGCCTCTGAGCTACCTCGACTTTGGACAGAG
TAATGACTCCCCAGAAAACGTCATATAAGACTTTACCAGCCCCTGAGAGGACCAGG
AGGAGCATCCTTGACCTTCATTTAACTTGGCTCACTTCTCTTCANACTTGGGTAGA
AGTGCAGAGCCACAAAATTGCTTTCCTTCCCCGCCTTTGACATGAGGCCTTCAGTA
AAG
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35

Sequence ID 611
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TGCAGGATCCGTCGACT
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Sequence ID - 612   nt: 576

GAGAAATATAAGATTATGTATAGATCAAATCTACCTCTATTTGGTGTCCTGAAAGA
GATGAGGAGAATGGGACAAACTTGGAAAGCTTATTTCAAGATAACATTCCTGAGAA
CTTCCCCAATCTTGCTAGAGAGGCCAACATTAAAATTCAGTAAATGCTGAAAACTC
CAGTAAGATATTTCTTAAGAAAATTATTCCCAAGATATATACTCATCAAATTATCT
AAGGTCAAATGAAGGAAAAAATTTTATAGGCAGCTAGAGAGAAATGTCAGGTCACC
TACAAAGAGAATGGCATAAGACAAAAGTAGAACTCCCAGCAGAAACTCTAAAAGC
CAGAAGAGATTAGGGGCCAATATTTAACATTCTGAAAGAAATTCCAACAAGGAATT
TCATATCCAGCCAAACTAAGCTTCATAATTGAAGGAGAAATAAGATATTTTCCAGA
CAAGCAAATGCTGATGAAATCCATCACCACCAGACCTGCCTTATAAGAGCTCCTGA
GGGAAGCACTAAATATTGAAAGGGAAGAACTTTATGAACCATTTCAAAAACACATT
TAAGTNCACAAAGCAG

Sequence ID - 613   nt: 341

CCTTATTTTACAGGTGAAAAACCACGAATCAGATAGATTTTTATTTGCCCAAGTCA
CATAATATTAAGAACAGGCCAAGTGTGGTGGCTCATGTCTGTAATCTGAGCACTTT
GGGAGGCTAAGGCGGGTGGATTTCCTGAGCCTAGGAGTTTGAGATCAGCCTGGGCA
ACATGGCGAAACCTCATCTCTACAAAACATACAAAAATTAGTCAGTGTGGTGGTGA
GAGCCTGTAGTCCTGGCTACTCGTGAGGCTGAGGTGGGAGCATCACCTGAGCCTGG
GAAGTCGAGGCTGCAGTGGCAACAGAATGGGTAACCTGGACATCAGAGTGAGACCC
TGTCT

Sequence ID 614

CTCACACCTGTAATTCCATTACTTTGGAAGGCTGAGAGAGGAGGATCAGTGGAGCC
CAGGAGTTTGAGACCAGCCTGGGCAATATAGGGAGACCCTGTCTCTACAAAAATGA
AATAGCCAGGCGAGGTGGCATGTGCCTGTGGTCCCAGCTACTTGGGAGACTGAGGT
GGAAGGCTGCCTTGAGCCCAGGAGTTCCAGGCTGCAGTGAGCCATCATTATGCCAC
TGCACTCCAACCTGGGAGACAGAGTGAGAGAGACCCTGTCTCAAACAAACAAACCC
AAAATAGGCCAGGCACAGTGACTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGA
AATAGGCGGATCATTTGAGGTCAGGAGTTCAAATTCAAGACCAGCCCGGCCAACAT
GGCAAAACCACATCTCTACTACAAATAAAAAATTAGTTGGGTGTGGNGGAGCATTC
CTGTAATCACAGCTATTCAGGAGGCTGAGGCATGANAACCGCTTCA

Sequence ID - 615   nt: 379

TAAATTTAAAACATTTTAATTAGCTGGCATGATGGCATGCACCTGTAGTCCTACCT
ACTTGGGAGGCCAAGGCAGGAAGATTGCTTGAGCCCAGGAGTTTGAGCTTACTGTG
AGCTGTGATCACACCACTGCACTCCAGCCTGGGTGACAAAGGAAGACCGTATTTCT

- 189 -

AAAAAATAAAAAATACAAATACAACTACAAACTAGCACTAGACCAACAGTGACTAT
GTACCATGAACTGAGGAATATTATTAATTCCACCATTTGCATCTGAGGTTAACAAT
ATGTCAATGACTTAAATAACATCATATCTCTGAGAGTAATTTCTCCTATATTTCCA
TGACAAATGTTAGATAATTTTCCATTTTTTCCATTCAACAAAA

Sequence ID 617

TTTTCAGGCATGTCAGAGAAGGGAGGACTCACTAGAATTAGCAAACAAAACCACCC
TGACATCCTCCTTCAGGAACACGGGGAGCAGAGGCCAAAGCACTAAGGGGAGGGCG
CATACCCGAGACGATTGTATGAAGAAAATATGGAGGAACTGTTACATGTTCGGTAC
TAAGTCATTTTCAGGGGATTGAAAGACTATTGCTGGATTTCATGATGCTGACTGGC
GTTAGCTGATTAACCCATGTAAATAGGCACTTAAATAGAAGCAGGAAAGGGAGACA
AAGACTGGCTTCTGGACTTCCTCCCTGATCCCCACTCTTACTCATCACCTGCAGTG
GCCAGAATTAGGGACTCAGAATCAAACCAGTGTAAGGCAGTGCTGGCTGCCATTGC
CTGGTCACATTGAAATTGGTGGCTTCATT

Sequence ID - 618   nt: 598

GATTAACTTTCATTTTAAGCTCTTCTCTACTAATTCTGTTCGTATGTTTATTCATT
TTGCGTTGATCATATTTTGTACACCAGGCACTCTTCTCAGTTTTATATGTGTGTTA
ATTTACTCCTTTCAAGAGCCCTATGATACATGAATTTATCTCCATTTTATAGATGA
GGAAATTAAGACCTAGAGTTACTGAACTTGCCCAAGGTTATACAGCTGATGGGTAG
GGCCAGAACTTTGCCTCAGAGAATCTGAATTTCCAAAAAATAACCTAAAAGAGAAA
TTTAAGTACTAATTAGTAAGCAAAGAAATGCACATTTAAGGAAGACAGTGCACATT
TAAGGAAGACAGTAACCTTTTATCTATTAGAGAAAAACACACATTCTGTCTTTAAC
ACACACATAAATCTTATATTGGCAGGGATTTTCTTTATTCAGCAATTATTTATTGG
TTGTCTGCTTTGTGGTACACATAAATGCTGGGGATAAACACTTAATAAAATATACT
TCCTTCTCTTGAATATCTTGCACTTTAAGTGGGAAGGTAAGTCAACAGAGTAGAGG
TGATATATCCAAGTGATAGACTGTTTCATTGCCAGTAG

Sequence ID 619

GTTGCCTGAGAGTGACCTTTGCATCTGCCTGTCCAGCCAGCATGGAACCAAAGCGG
ATCAGAGAGGGCTACCTTGTGAAGAAGGGGAGCGTGTTCAATACGTGGAAACCCAT
GTGGGTTGTATTGTTAGAAGATGGAATTGAATTCTATAAGAAGAAAAGTGACAACA
GCCCCAAAGGAATGATCCCGCTGAAAGGGAGCACTCTGACTAGCCCTTGTCAAGAC
TTTGGCAAAAGGATGTTTGTGTTTAAGATCACTATGACCAAACAGCAGGACCACTT
CTTCCAGGCAGCCTTCCTGGAGGAGAGAGATGCCTGGGTTCGGGATATCAATAAGG
CCATTAAATGCATTGAAGGAGGCCAGAAATTTGCCAGGAAATCTACCAGGAGGTCC
ATTCGACTGCCAGAAACCATTGACTTAGGTGCCTTATATTTGTCCATGAAAGACAC

- 190 -

TGAAAAAGGAATAAAAGAACTGAAT

Sequence ID 621
TGGTACTGAACCTACGAGTACACCGACTACGGCGGACTAATCTTCAACTCCTACAT
ACTTCCCCCATTATTCCTAGAACCAGGCGACCTGCGACTCCTTGACGTTGACAATC
GAGTAGTACTCCCGATTGAAGCCCCCATTCGTATAATAATTACATCACAAGACGTC
TTGCACTCATGAGCTGTCCCCACATTAGGCTTAAAAACAGATGCAATTCCCGGACG
TCTAAACCAAACCACTTTCACCGCTACACGACCGGGGGTATACTACGGTCAATGCT
CTGAAATCTGTGGAGCAAACCACAGTTTCATGCCCATCGTCCTAGAATTAATTCCC
CTAAAAATCTTTGAAATAGGGCCCGTATTTACCCTATAGCACCCCCTCTACCCCCT

Sequence ID 622
TTTTTCTTGTTTTTGTGTGTCTACCTTGGCATATACTAAAGGAAGGTGTGTATTCA
TTTATTACATGATATCTCTGGGTTATAATTATTTACATATATGAATTTGAAAGAAA
GATTGAGAGGGATATGTGTGACCTTTGTTTCATTATGATCATTTACATGACTAAAG
ATAAAGATCATATGTCTGATTTTCAGTTTAATGGCAAGTTACTTAAAATAAATGAA
ATATGTTTTTATTGTTTTCGTGGGTTTGATGCTTTGTGTTTTATTTCAAGTAACTT
GAGAATGCATTGTGTTTGGTACTGTTTTTTATGAATATCATTAAAAATTTATTTAA
GGAGAGAGTAATTTTGCAATAATATTTTTGATTTATTTGAAAATAAAATTCAAGAT
AAATGAAATAATTGAAATTTTCTAAAGAAGGAATTGAATATATTTTTACATTTGAA
TGAACTAAGGATTAACTGAACCATTTATATATAGTACTTTCAGAACTGAATGTCTT
AAATGATAAAGCTCTAATTGGTTAAAGTGACTTTCTTTCAAGTCAAAGAACCCAGA
AACTGAATAGATGATCTAACTACTGCCACTGAGGTTTTGGATTAGTGAGTATAAAT
TT

Sequence ID 624
TGCAGGATCCGTCGACT

Sequence ID 625
GACAATCAGAGCAGATCTTGGGCTTCTGTGGCTCATCTCAGCCCTTTATAACTGGC
CTGAGAAGAGGGTTTATCTACTTGTGCAAGTGGCCCAGAAATCTCACTCGTACATG
AGGCTTTGGAACATCCTTGCAAAGGTACGCTGAAAGCAAATTGCTGTTTTCCTGGT
GGTTCTGCACGTTTCCTAACTTTTATCATAGTTTGATTTTCATTATTTAAGAAAAA
ATAAAAAATCCAAAGACCATAAGATGGCATTAGATTTTTTACCATTAAATTATTAA
TGCCTATTTGGTGCTCATAAAGATTAATCATGTCACGCATGTTTCCAATCTTTCTT
TTGCAGTATATTATTTTCTAAAAATTGTTACATGCAAATTTAAACCAAGATTTATC
AGTA

- 191 -

Sequence ID 626

TTGGAAGAAATAAACCAAGGCAGAAAAATTTTAAATGGCCAAAATAAATTGTATTG

CTAACTTAGATGGCCACAGATGGGGGCAGGGGTGGAGAGAGGAGAAATTGAAAACN

CCACAAAGACCCCGCAATGGCTAGAACTTGAAATCTCTGGATATTGCAACAATAGC

5   AGCCTCCTTAAGTCAGCAAAAAGATAAAGATTGATCCAATGTTCTATATTACAGAA

CAGAGCAGATTGTCAATATAGCAAATAAAGTTACCGTTGAGTGGACTGCGCTGTNT

AAGCTGCTTGGTTGGCCTTAAGTGCCGACAATTAAGAGATGAAGGCAATGAGAACT

GAAACAAACATTTAAGTTCAAGACCCAGTTTACTGACACTGGGACTATTACTATAT

CTCTTTGGGCCTCAGTTTACTTATCTGTAACATTAAGAGGTTGGATTACATGATGT

10   CTCACGATTCTTTTTTTTTATTTAGAGATGGGGTTTTGCTCTGTTGCCCAGGCTGG

AGTGCAGTGGCATGATCATAGCTCACAGCAG

Sequence ID 627

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15   ACTCTACTGGCCACACTGTGTGGCCTGAGACCCCCCTTTCCCTCCCAAGCCCCTGC

CTCCGCATCTGCGTGGTGAAGGCCATTGGCCCTCATCGGTGGATCTGCGTTTCCTC

GGGCCTACACTGTCTAGGATTGTGCGGGGCTGGTGAGAGAACAAGATCTCTTCCGT

GTTCAAGGCAGACTTCCTGCCCCCTGCACCCTGCTCTCTCCCAGGCCTTGAGGTCA

GTGTGAGCCCCAAGGGCAAGAACACTTCTGGAAGGGAGAGTGGATTTGGCTGGGCC

20   ATCTGGATGGAAGGTAAAAAAAGAAAATCCCTTGAAAGGAGATTGAGGGAAGTTT

Sequence ID - 628   nt: 419

AAGAGAAAGGACTCAGTGTGTGATCCGGTTTCTTTTTGCTCGCCCCTGTTTTTTGT

AGAATCTCTTCATGCTTGACATACCTACCAGTATTATTCCCGACGACACATATACA

25   TATGAGAATATACCTTATTTATTTTTGTGTAGGTGTCTGCCTTCACAAATGTCATT

GTCTACTCCTAGAAGAACCAAATACCTCAATTTTTGTTTTTGAGTACTGTACTATC

CTGTAAATATATCTTAAGCAGGTTTGTTTTCAGCACTGATGGAAAATACCAGTGTT

GGGTTTTTTTTTAGTTGCCAACAGTTGTATGTTTGCTGATTATTTATGACCTGAAA

TAATATATTTCTTCTTCTAAGAAGACATTTTGTTACATAAGGATGACTTTTTTATA

30   CAATGGGAATAAATTATGGCATTTTTT

Sequence ID 629

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GCATGCTGTAGCCAGCTCCTTAAAGGAAGGATGGTGCCTGGTACAGAGTTAGAGTT

35   AGTGCTTCAGTAAATAATGAATGTGTGCTAGGTAGGTTCTGCTGGGTAGGCTGCAT

GCATTGACCAATTTATTCCTCCTTGTTTCAAAACAGGATTTAAGGGCACTTATATA

TATATATTTTTTAGTTTTTTTAATGTAAATGAGAGAATAAAGATATATATATATGT

CTATATATGTATATATGTATATATATGTCTATATGTCTATATGTATATATGTCTAT
ATGTATATATGTGTGTGTATATATATATATATATATATAAGTTTTCTGTTGCTA
GCATAACAAACTACCAGAAACTTAGCAACTGAAACAACATGAATTTATCTTACGGT
TCTATAGTTCAGAAGTCTAACGTGTCACTGGGATGAAATCCAGGTTTCAACAGGAC
5   TGGGTTCCCTTCTAGCTCATTCAGCTACCTGGCTCATTCAGGTTGTNGGCAGAATA
TACTTCCATGAAACTGTAGGGCTGAGACCCCGTTCCTTCCTGGCTATCATCTGAAA
ACTTTC

     Sequence ID 630
10   AGGCGCAGCCCAGCCTCGAAATGCAGAACGACGCCGGCGAGTTCGTGGACCTGTAC
GTGCCGCGGAAATGCTCCGCTAGCAATCGCATCATCGGTGCCAAGGACCACGCATC
CATCCAGATGAACGTGGCCGAGGTTGACAAGGTCACAGGCAGGTTTAATGGCCAGT
TTAAAACTTATGCTATCTGCGGGGCCATTCGTAGGATGGGTGAGTCAGATGATTCC
ATTCTCCGATTGGCCAAGGCCGATGGCATCGTCTCAAAGAACTTTTGACTGGAGAG
15   AATCACAGATGTGGAATATTTGTCATAAATAAATAATGAAAACCTAAAAAAAAAAA
AAAAAAAAAAAAA

     Sequence ID 631
TNCACTCACACACTCCCAAACCTTAACAAACACATACATGTGCAGCCAACCCAATG
20   GGCCAGCCTCTTTTATGCTCCTCACATGTTTCCTTTAACTGGAATACCCATGACAG
CTCCCTACATAGTTACTTGTAAACTCCTCCTCTCTGTATAAGTTTTCCTGAATTTT
TTTGATAAAATTAAGTTGTGCCACCCCTTTATGCTCTCTTANAACTTTGTTCTGTT
CTCATGGCTGTTCTGCAACGAATCTCATTGTGTTCTCCTACTCAATTACATTCCTG
CGTCTCCCACTAGATGGCAGACTCTTTGAGAGTAGGAGATTCCCTTGTTATCTCTG
25   GATCCCTGGCACTTGCAGAAAGCCTGTTACGTAATAATTGCTCAACAATTAGTTTT
TAAATAAATGAATTATTTTTAAAACGCCAAAATTACAATGATTGTGCATTAAGTGA
AAGATGACCATCTAAAAACATAAAGCCATGCTTCATGACATTGGC

     Sequence ID 632
30   GACCATTCAGGGAAATTTTATAAAAAATGCAGATACTGTCTTGAGCAGATCGAAAT
GCCGATGAGGTGGATGCAATTTCCTTTTGTGCAAGCAGTGCACGGTGCCCCCCCCT
CGGGTGTCCGTGCTGTGCCTTAGCTTCCCCAGGTGCCGGGACTCACACCTGCTAGG
GGCTGGGCAAGGCCCCGGCTCTGCTTTCTCTGAAGGGCTTGTCCAAGTTCATTGCC
CTGTTACAGGTGGTCAAGACGTCCGGCCGCCTTGACCCAGGCTACCCTTAGCCAAT
35   ATCCTCTGCCCCTGGGTGGTTGGTGGCTGGGCCTCAGGGTGGGCAACGTTAGGGGT
TTGGCGAAAGCCCGCCCCATGGGATTGAGGGACGGGGCTGCACTCCAACCGTCTGC
ACCTGCTCTTCCCCCACCCCTGTGGGACCTCATCTTCACGTGCCATGTGTGCTGAA

- 193 -

GGCCCAGGGCCCAGCAGGGGGCAGTGGCACCTGTTGACGGAAAAGCCGAGGTGCTT
ACCAATGGACCTTCTGGCCCGCCCTCCCCTGTACTTGTCGGGCATTCAGGGCCCCG
ACCTGTGCCTACCCGCA

5   Sequence ID 633

CAACTGTGTTCACTAGCAACCTCAAACAGACACCATGGTGCACCTGACTCCTGAGG
AGAAGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAAGTTGGTGGT
GAGGCCCTGGGCAGGCTGCTGGTGGTCTACCCTTGGACCCAGAGGTTCTTTGAGTC
CTTTGGGGATCTGTCCACTCCTGATGCTGTTATGGGCAACCCTAAGGTGAAGGCTC

10   ATGGCAAGAAAGTGCTCGGTGCCTTTAGTGATGGCCTGGCTCACCTGGACAACCTC
AAGGGCACCTTTGCCACACTGAGTGAGCTGCACTGTGACAAGCTGCACGTGGATCC
TGAGAACTTCAGGCTCCTGGGCAACGTGCTGGTCTGTGTGCTGGCCCATCACTTTG
GCAAAGAATTCACCCCACCAGTGCAGGCTGCCTATCANAAAGTGGTGGCTGGTGTG
GGCTAATGCCTGGCCCCACAAGTATCACTAAGCTCGCTTTCTTGCTGTCCAATTTC

15   TATTAAAGGTTCCTTTGTTCCCTAAGTCCAACTACTAAACTGGGGGATATTATGAA
GGGCCTTG

Sequence ID - 634   nt: 511

TTTTTTAATTTCACCAAAATTTGTTGACGTCCCTTGATTTGCTGATAGGGACAATA

20   ATTAAATATTTTCCACTTGTTTTTATAAAAACTGTAATGGTGATTTGTTTAACAGA
TGTTGACTTAGCACCTTCTCTCTTTTTTTTTTTTTTTTTGAGTTGGAGTCTTGC
TCTGTCACCCAGCTGGAGTGCAGTGGCACGATTTCGGCTCACTGCAACCTCCGCCT
CCCAGGTTCGGGCGCTTCTCCTGCCTCAGCCTCCCANATAGTTGGGATTACAGGTG
CATGCCGCCACNCCTAGCTAATGTTTTTTGTATCTTGGTANANATGGNGTTTCACC

25   TTGTTGCCCATGCCGCTCTTGAACTCCTTGGCCTCCCAAAGTGTTAGGATTACAGG
CGTGAGCCACTGTGCCTGGCCCCAATTTANCACCTTACTGGGTGCTGAGGCTGTGA
GCCATAGTAGAATGCATGTGATCCAGGGCCTTGCTGAATTCATGGGCTAATAGGGA
GCCTGAC

30   Sequence ID - 635   nt: 592

TGAGCGTTGGGCTGTAGGTCGCTGTGCTGTGTGATCCCCCAGAGCCATGCCCGAGA
TAGTGGATACCTGTTCGTTGGCCTCTCCGGCTTCCGTCTGCCGGACCAAGCACCTG
CACCTGCGCTGCAGCGTCGACTTTACTCGCCGGACGCTGACCGGGACTGCTGCTCT
CACGGTCCAGTCTCAGGAGGACAATCTGCGCAGCCTGGTTTTGGATACAAAGGACC

35   TTACAATAGAAAAGTAGTGATCAATGGACAAGAAGTCAAATATGCTCTTGGAGAA
AGACAAAGTTACAAGGGATCGCCAATGGAAATCTCTCTTCCTATCGCTTTGAGCAA
AAATCAAGAAATTGTTATAGAAATTTCTTTTGAGACCTCTCCAAAATCTTCTGCTC

- 194 -

TCCAGTGGCTCACTCCTGAACAGACTTCTGGGAAGGAACACCCATATCTCTTTAGT
CAGTGCCAGGCCATCCACTGCAGAGCAATCCTTCCTTGTCAGGACACTCCTTCTGN
GAAATTAACCTATACTGCAGAGGTGTCTGTCCCTAAAGAACTGGTGGCACTTATGA
GTGCTATTCGTGATGGAGAAACACCTGACCCA

5

Sequence ID - 636   nt: 572
CTTANAAGAGTTGCTCATTCACACCCACGCCCTTGCCCAAGGCTGGCCCACTCAGA
GCGAAACTTAACTTTTGTCTGGATGGGAAGAGAAGTAAGTCTACCCCGAGGTTGCC
ATGTTGAAGAGTGAGAGGTCCAAGTGATTCTGTGCATTGAAACCAAGACACCCCAC
10   CCAGAACACTTCTTCCCTCCCTCAGCCCAAACCAAAGGCTGGGGTTCTCATCTCCA
    AGTGGCTGTTCTCCAACTTTCCCAAGCCGCTTGCATTCCCCAGACTGGACTACTGT
    GGCGGTTAGGTTAGATTTGAAGACGGGGCCCAGGCTGGGTATGAACGGGTGCAGCC
    CTCTTCTCCTCTTCCCCCCCACATCTCTCATGAGAGAGGTAGTGGCATTTCCTTCT
    CAGGGAGCTTCAATGGGAAAGGTCTCGAAAGCTTCAGGAGGAGCAGAATACCAACG
15   CAGGGGGATGGCTGTAACGATCTCACCGTCTCCTAACCTCAGTCCCTTTTTTGAGA
    GTGAATGGTGGAGGGTGGGAAAGGGACCCAAATTTGTAGATCTCTTTGTCTGGGGG
    AGGGGAANGATG

Sequence ID - 637   nt: 482
20   TTAAAACAGGCGCAGGGGTAAAAATGAGAATGAATCTGAAAAAAGAGAGTTGGTGT
    TTAAAGAGGATGGACAAGAGTATGCTCAGGTAATCAAAATGTTGGGAAATGGACGA
    TTGGAAGCATTGTGTTTTGATGGTGTAAAGAGGTTATGCCATATCAGAGGGAAATT
    GAGAAAAAAGGTTTGGATAAATACATCAGACATTATATTGGTTGGTCTACGGGACT
    ATCAGGATAACAAAGCTGATGTAATTTTAAAGTACAATGCAGATGAAGCTAGAAGC
25   CTGAAGGCATATGGCGAGCTTCCAGAACATGCTAAAATCAATGAAACAGACACATT
    TGGTCCTGGAGATGATGATGAAATCCAGTTTGACGATATTGGAGATGATGATGAAG
    ACATTGATGATATCTAAATTGAACCAAGTGTTTTTACATGACAAGTTCTCTGAGGA
    TGGTTCTACAGTTGGGATTTTGGCCATCATCAAC

30   Sequence ID - 638   nt: 545
    TTTGAAGGCAAAGAGGGATTAATCTGTGCTGGCATCATGTAAGGAGACTTGATAGA
    TAAGAAAAAGCTTTACCTAAGTTTTGAAGAATAGGTTTTTCATAATGGAAAATTTA
    AGGGAAAAATCTCCAAAAAAGTGCTACTCAAGTTTTATCCATTTGTATTTCCAACA
    CAGCCTAGGACAGTACCTGCACATAGTAGGTGATTAATAAAAATTTAGAAAGCATT
35   AATACTAAAGAGGAAAAATAGCAATGGCAAGAAAACACATGTAGGGAACACATGTA
    GCCAAAAAATAATATATAATCAGAGAAATAATAGGACTTCTGGAAAAAAAAGATGA
    GATCAGATTGGTTAGGATCTTTACTAACATGACAAGAGCATGAATTTTTTTTCTGT

- 195 -

AGATAATAAGTATGAAAGAATTTTAGCTTAAAAATTAGCATAATTTGGATCCACAT
ATGCAAATCAATGAATGTAATTCATAATATAAACAGAACTAAACACAAAAACCACG
TGATTATCTCAATAGACACAGAAAAGGCCTTCAAAAAATT

5   Sequence ID - 639   nt: 624

GACACACGAGCATATTTCACCTCCGCTACCATAATCATCGCTATCCCCACCGGCGT
CAAAGTATTTAGCTGACTCGCCACACTCCACGGAAGCAATATGAAATGATCTGCTG
CAGTGCTCTGAGCCCTAGGATTCATCTTTCTTTTCACCGTAGGTGGCCTGACTGGC
ATTGTATTAGCAAACTCATCACTAGACATCGTACTACACGACACGTACTACGTTGT
10   AGCCCACTTCCACTATGTCCTATCAATAGGAGCTGTATTTGCCATCATAGGAGGCT
TCATTCACTGATTTCCCCTATTCTCAGGCTACACCCTAGACCAAACCTACGCCAAA
ATCCATTTCACTATCATATTCATCGGCGTAAATCTAACTTTCTTCCCACAACACTT
TCTCGGCCTATCCGGAATGCCCCGACGTTACTCGGACTACCCCGATGCATACACCA
CATGAAACATCCTATCATCTGTAGGCTCATTCATTTCTCTAACAGCAGTAATATTA
15   ATAATTTTCATGATTTGAGAAGCCTTCGCTTCGAAGCGAAAGTCCTAATAGTAGA
AGAACCCTCCATAAACCTGGAGTGACTATATGGATGCCCCCACCCTACCACACAT
TCGAAGAA

        Sequence ID 641
20   CAAGATGACAAAGAAAGAAGGAACAATGGTCGTGCCAAAAAGGGCCGCGGCCACG
TGCAGCCTATTCGCTGCACTAACTGTGCCCGATGCGTGCCCAAGGACAAGGCCATT
AAGAAATTCGTCATTCGAAACATAGTGGAGGCCGCAGCAGTCAGGGACATTTCTGA
AGCGAGCGTCTTCGATGCCTATGTGCTTCCCAAGCTGTATGTGAAGCTACATTACT
GTGTGAGTTGTGCAATTCACAGCAAAGTAGTCAGGAATCGATCTCGTGAAGCCCGC
25   AAGGACCGAACACCCCCACCCCGATTTAGACCTGCGGGTGCTGCCCCACGTCCCCC
ACCAAAGCCCATGTAAGGAGCTGAGTTCTTAAAGACTGAAGACAGGCTATTCTCTG
GAGAAAAATAAAATGGAAATTGTACTTAA

        Sequence ID 642
30   TGCTTGGCCCTCTACCTCCTGCCCTCTTCCTGTTCATCTCCCAACCACTGCACTCT
TGATTTTTATACCACACAGAAGGTAAGAAAATTCTAGGAACCCTAAGGATCAATCC
TCTCCATTTTCACTCAAATGCCTGGGGCCCAGCTCTGCAATGACTGACTCCAGGGC
CTCTTTCCTCACTGCCAGCATAGAAGTCAGGGGAGCCAGCTGGGCCCTGCGGTCAG
GAAGGTTCTCATTTTTGGAGCATTCCCTGAGCCCAGATCATAGGAGCAGCTGTCCC
35   TGGTGGGACACAGGAGTCATGACTCCTACCCTCCACCCTCCACACCCACCAGGCAT
TTAGCAGTCTGTCCTATGCAAGACAGATGAATTCTCAGCCAGGATACCTCAAGGCA
GGCAAAGGTGAGTGGAGGGAAAATTCACAAACATTCAGGGTGTGTGGTGCTGGCAT

CACCATGGCCAAATCCAAGAGGTCTTCCTGGAAGAGGGCCCAAACTGGAACCAAAA
GAATGCTGTCAGCAGTTGGAATAGAGCTGTGAATT

Sequence ID 643

5

CTTTCCAAGAGGAATCCTCGGCAGATAAACTGGACTGTCCTCTACAGAAGGAAGCA
CAAAAAGGGACAGTCGGAAGAAATTCAAAAGAAAAGAACCCGCCGAGCAGTCAAAT
TCCAGAGGGCCATTACTGGTGCATCTCTTGCTGATATAATGGCCAAGAGGAATCAG
AAACCTGAAGTTAGAAAGGCTCAACGAGAACAAGCTATCAGGGCTGCTAAGGAAGC

10   AAAAAAGGCTAAGCAAGCATCTAAAAAGACTGCAATGGCTGCTGCTAAGGCACCTA
CAAAGGCAGCACCTAAGCAAAAGATTGTGAAGCCTGTGAAAGTTTCAGCTCCCCGA
GTTGGTGGAAAACGCTAAACTGGCAGATTAGATTTTTAAATAAAGATTGGATTATA
ACTCT

15   Sequence ID 644
CTTTGATAGAGAAGAAAATTCTCCTAGGATACAAGAGCCTCAACATTTTAAAGATT
TTCTGCATCTCAAAAGCGTAGGCTCCTTGCTGGGCAAGGTGAGCCTCTGTGAGTCC
TCATAGGACCGAGCAAATCTGATTCACCCCAGAAAATCCAATATCGAAGCTGAGCT
TTGGCCTGAGCGGGTTCCATTTCCTCCCCAGATCCTATTTAGGAAGTGTCTCCTGA

20   CAACCTCCAAAAGGTGCTAACATGCAACGTTCTGAAGGGTTATTGCTCAAAAACAA
GATTTTCCTTGTGGTCAAGACTCTGCGAGCCTCGAACACGATGAATCCGCTCGAAT
GGGCTTGGGCTTTGCCCGGGTGGCGCACGCTCACACGCTGGAAGCACAGCTTTGAC
GATCTCCACACACGCACAGGCACACACGCCACAGATGATGCCGGCTCATTCTCAGG
GGGTGTCTAAGTTCTGCTTTAAATATTTACCCCCTAATTGTACAAACAATAGGGGC

25   ATGAGCCTGGTACTCGATAAATGGGGACTTNCTTAAAA

Sequence ID - 645   nt: 649
CTACAGCCTGGGCAGCGCGCTGCGCCCCAGCACCAGCCGCAGCCTCTACGCCTCGT
CCCCGGGCGGCGTGTATGCCACGCGCTCCTCTGCCGTGCGCCTGCGGAGCAGCGTG

30   CCCGGGGTGCGGCTCCTGCAGGACTCGGTGGACTTCTCGCTGGCCGACGCCATCAA
CACCGAGTTCAAGAACACCCGCACCAACGAGAAGGTGGAGCTGCAGGAGCTGAATG
ACCGCTTCGCCAACTACATCGACAAGGTGCGCTTCCTGGAGCAGCAGAATAAGATC
CTGCTGGCCGAGCTCGAGCAGCTCAAGGGCCAAGGCAAGTCGCGCCTGGGGGACCT
CTACGAGGAGGAGATGCGGGAGCTGCGCCGGCAGGTGGACCAGCTAACCAACGACA

35   AAGCCCGCGTCGAGGTGGAGCGCGACAACCTGGCCGAGGACATCATGCGCCTCCGG
GAGAAATTGCAGGAGGAGATGCTTCAGAGAGAGGAAGCCGAAAACACCCTGCAATC
TTTCAGACAGGAAATCCAGGAGCTGCAGGCTCAGATTCAGGAACAGCATGTCCAAA

TCGATGTGGATGTTTCCAAGCCTGACCTCACGGCTGCCTTGCGTGACGTACGTANC
AATATGAAAGTGTGGCTGCCAAAAACCTTGCAG

Sequence ID - 646   nt: 600
GAGATGTCTCGCTCCGTGGCCTTAGCTGTGCTCGCGCTACTCTCTCTTTCTGGCCT
GGAGGCTATCCAGCGTACTCCAAAGATTCAGGTTTACTCACGTCATCCAGCAGAGA
ATGGAAAGTCAAATTTCCTGAATTGCTATGTGTCTGGGTTTCATCCATCCGACATT
GAAGTTGACTTACTGAAGAATGGAGAGAGAATTGAAAAAGTGGAGCATTCAGACTT
GTCTTTCAGCAAGGACTGGTCTTTCTATCTCTTGTACTACACTGAATTCACCCCCA
CTGAAAAAGATGAGTATGCCTGCCGTGTGAACCATGTGACTTTGTCACAGCCCAAG
ATAGTTAAGTGGGATCGAGACATGTAAGCAGCATCATGGAGGTTTGAAGATGCCGC
ATTTGGATTGGATGAATTCCAAATTCTGCTTGCTTGCTTTTTAATATTGATATGCT
TATACACTTACACTTTATGCACAAAATGTAGGGTTATAATAATGTTAACATGGACA
TGATCTTCTTTATAATTCTACTTTGAGTGCTGTCTCCATGTTTGATGTATCTGAGC
AGGGTGCTCCACAGGTAGCTCTAGGAGGGCTGGCAACTTA

Sequence ID 647
CGAATGTGCAGGTTTGTTACATAGGTATATATATGCCATGATGGAAATATTTATTT
TTTTAAGCGTAATTTTGCCAAATAATAAAAACAGAAGGAAATTGAGATTAGAGGGA
GGTGTTTAAAGAGAGGTTATAGAGTAGAAGATTTGATGCTGGAGAGGTTAAGGTGC
AATAAGAATTTAGGGAGAAATGTTGTTCATTATTGGAGGGTAAATGATGTGGTGCC
TGAGGTCTGTACGTTACCTCTTAACAATTTCTGTCCTTCAGATGGAAACTCTTTAA
CTTCTCGTAAAAGTCATATACCTATATAATAAAGCTACTGATTTCCAAAAA

Sequence ID 648
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

Sequence ID - 649   nt: 425
CAAAAAAACGAAGAAAAGTGACGACAGTCTGAGGGACTTATGGGAGATCATCAAGT
GAACCACTATATGTGTAATGTAAGTCTTGGAATGAGAAGAGAGAAGGAGAAGGAGG
AGAGAGCTTATTTGTAGAAATAATGGCTGAAAACATCCCAAACTTTCCTTTTTTTG
AGGAAAGAAATAGGCATACAAGTTCAAGAAACTCAAGGAACTCCAGAGAGGACAAT
TCTAAAGACACCCCCTCTAACATACATTATAATCAAATTGTCAAAAGTAAAATACA
AAGAGAATCTTTTAAATTGACAAGAGAAAGCAGCTGGTCACGTTCAAGGGAGTTC
TATAAGAATTTCAGCAGATTTCTCAGCAGAAACCTTGCAGGCCAACAGGCAGTGGG
ATGATACATTCAAAGTGCAAAAAAAAAAAAAAA

Sequence ID 650

CGAGAGTTTACCAGTNGCCTAATAATGCAATAAAAAATGCTTTGAGATAGCTAACN
GCCCATAAAACAAACTCAAATTGCTTATAAAGTTTCTTCCCATGTTCCCATTTGAT
'GAAAAGTCTTACATCACATATAACTGGGAAGCAGGGGTCCCTCCTCAATTTTCAGA
CATTTTGAAAGGATGACAGTTCTGTTTGTTAGATGAGTAAACCTCTATATTCATAA
GTTCTAAAATCCTTCATTATGAGGGATTCAAAGTATTTATAAAAACACTGCCCTCT
AAAAATTTCCTCAGATCTGAAGTATGGNCTTGGNCCTGAATATACAGTGTTATCCT
ATGTTTAAAAGGGTGATCCAGACATGAGACGCAACTAGTTGGTGCATAAGAAGGCC
CCACTTGGCTATTTCATATCTACCTACAATTGACCAAAAAAATTTTTTAGGCCAG
CAATTATTATTTAGCTTCGCTCTTTCTAGTGCAAGAAACTGCAGGCTGGATCAGTA
GTTCAACAGCTAAACAGTCATAAAATAGTCATTGGCATGTTAAATTTCTTTCAATG
CTTCAAAGATAAATTCCAATTCTATTTACTTATTCATTGNGACNGNATTACTAAAC
AGGTAAGGATGGGAATA

Sequence ID - 651   nt: 251

CTTTGGGAGGCCGAGGCGGGCGGATCACTTGAGGTCAGGGGTTCGAGACCAGTCTG
GCCAACATGGTGAAACCCCAACTCTACTAAAAATACAAAAGTTAGCCAAGTGTGGT
GGCAAGTGCCTGTAATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATCACTTTGA
ACCTGGGAGGCGGAGGTTGCAGTGAGCCAAGATCGTGCCACTGCACTTCAGCCTGG
GCAACAGAGCAAGATTCCGTCCATCTC

Sequence ID 652

CTTTCTTCAGCCTTGCAGACACCTAAACATCATGTAATTACCTAAGGAATTCCCAA
GTGCCTCTTCCAGGTTATACGTGTAAATAGCTGTTTTTATGCAAGATTAGTTAGAT
ACTGCTCTTTACAGGATGAGTGGTGTTGTCTTTGGCTGGGGGGGNCTTAAATGTGT
TTCTAATGTGTGTGTCAAATAATTACCTGTTAAACAGACTGCCAATCTGGCTGAAG
CCAATGCTTCTGAAGAAGATAAAATTAAAGCAATGATGTCGCAATCTGGCCATGAA
TACGACCCAATCAATTACATGAAGAAACCTCTAGGTCCACCACCTCCATCTTACAC
GTGTTTCCGTTGTGGTAAACCTGGACATTATATTAAGAATTGCCCAACAAATGGGG
ATAAAAACTTTGAATCTGGTCCTAGGATTAAAAGAGCACTGGAATTCCCAGAAGT
TTCATGATGGAAGTGAAAGATCCTAATATGAAAGGTGCAATGCTTACCAACACTGG
AAAATATGCAATCCAACTATAGATGCAGAAGCATATGCAATTGGGAAGAAAGAGAA
ACCTCCTTNTTACCAGAGAGCCATCTTNTTTCT

Sequence ID 653

GTTGTGACTCGTTGGCATGTGATCTGAAGTTCCTGCCCTGCAGCTGACGAGCCAGT
GTTTCAATAATTAAAAACAACTCAACTCACTGTCCTCCTGCCTTGAATTTGATCAT ·

TGCGCTTTGCATGTATGTATCACAATACCACATGTACCCCATAAATATGTACAAAG
ATTATGTGTCAATAAAAAACAAAAATTAAAATCCCAATTTTTA

Sequence ID 654

GTTGCTAGTAGCGGCAGGAAGATGTCAGGCTCACTTTCCTCTGATTCCCGAAATGG
GGGGAACCTCTAACCATAAAGGAATGGTAGAACAGTCCATTCCTCGGATCAGAGAA
AAATGCAGACATGGTGTCACCTGGATTTTTTTCTGCCCATGAATGTTGCCAGTCAG
TACCTGTCCTCCTTGTTTCTCTATTTTTGGTTATGAATGTTGGGGTTACCACCTGC
ATTTAGGGGAAAATTGTGTTCTG

Sequence ID 655

GTCCCCGGGAATCGCGGCCGCGTCGACGGTTTATTTTCAGTGCTTGAAGATACATT
CACAAATACTTGGTTTGGGAAGACACCGTTTAATTTTAAGTTAACTTGCATGTTGT
AAATGCGTTTTATGTTTAAATAAAGAGGAAAATTTTTTGAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAATTTTT

Sequence ID 656

TAGAGGCCTGAATAGGTAGACAATGGCAGCAGCGTTTTTAATCACAGTCCTATTCA
TGCCCTAATTCGGGAGTGATGATTAAAGGACATTAGAGGGAGCACTTTGACATCTG
ATCCTTTGAACTGACGTCTGTGCAGGCTGCACTCCATAGAGCTCACTTGGCCAAAC
TGATTTCCTTAAATAAAGTGCTGTGATTTCCAATGTAGGAAATATTACATTAGAGC
CTATTGAAATGATTAGGAATTGAGGAGCTTTTCTTTAGGTGGGAATGTGGTGTATG
CTGTATACTCACAAAGTGAGATCATTAATATTGCATGTACTACTTTGAATATCAG
GGACCACAGAGAAATAGCATGAGAAACGCCTTCCTGCAGTCATGCACTTAAAATGA
ATATGAACAAAAATGTGGAACTCTGCTGTCATAGCTCTCCG

Sequence ID 657

GGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGTTTTTTT
CTCTTTGAAAGATAGAGATTAATACAACTCTTAAAAAATATAGTCAATAGGTTACT
AAGATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAG
AGAAAATATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCT
AAAACATGACGGAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAA
AGAAAATTGAGAGAAAGGACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAAT
GCTTTTAGATTAAAATGAAGGTGACTTAAACAGCTTAAAGTTTA

Sequence ID 658

- 200 -

GACCTTTGAGAAAATTAATTTAAATCCTAGAACTTTGGGTGAACCGAAGAAATTTA
TAATATTTGTTTAGTTAATAACAGATAAAAAGGAAAGATTCAAGCCTATTGGATGA
GAATTTGTACATTATTTTAGAGCTAATAATAATGGTTTTCAGTTTAGTGAGGATTT
AAAAAATGTTTTTGAATCAAACTTTTTTTCTTTATAATCCTTTTTAACTAACTCAG

5   GAAATAAGGTATTATGAAATCCACACACTGTTACCTCCTTAAAGTATGAGGATACT
TCCCACTGTTTGGTCCACTAGTGGCTGATTATTTTGTTTGTGGATTATTTGTAATT
TTCTTTTTAATTCTTCCTTAAAGAGCATGGCATTTGGAGTCACAGACCTATATTTG
AATCCTGTCATTTACTAGCGTTTTGACCTTGAACAATTATGCTCAGAGTCTCAGTT
TTTTCTTGTAAAGTGATGATGATACTACTTAACTCACAGGGTTGTAGTGAAGATCA

10   AATGAGATCATGTCTGTANAACACCCTGCCCGGCACTCAATAAGTATTAATAGGAA
CCCATATACCTC

Sequence ID 660
TGTTTTTATTTTTTAAAAGGTATAAACACCAAAAAAAAAATTAACATTGTATGAAG

15   ATGGAAAATAAGAAGATGCACTTTCTGTAACTTTGTCTAAGGATTTAAATTACTAA
CTTATGAACTCCAATTTGAATTGAACTTAACTATCGGCTTTCTTACTGGTAAAATT
ATATGGTTTATTTTAAATGCGTACATATTGACCAATGGCCTCTGAAAAAGCACATT
TTAGATACTGAAATTGAAGGAAAGAAAATGCATCTTCAAACATTTTTTGGAATCTC
ACCACATATACTTTGTTANATTTGTGTATTGTAGGGTGTTTGTTTTGTATTTTTGT

20   ATTGTATATGAACTTTTTTTAAATGTGACAGTTAAACACATCTTTAAAAGCATAGT
CACAGACAAAAGCATACAGTATAAAAATTTCCTTGAAAACTCCTACAATATTATAT
TTGGAGGCAGCTTCAGACTGTTTTATTGG

Seqeunce ID 661

25   CTCTGGCACACATTAGTTCCTCTTATATTACATTGATATAAGCAAGTCATATGGAT
TTATCTGAGTGTAAGGAGAGCTGGAAAAAATAGTTTCTAGCAGGTCAGCCACCTCC
CAGTGAGGGCTGCATACCATAGAAGGGGAGAATGAATTTTGGGAAAACAGGTAATT
ATCTCTGTCACAGAAGGGGATGAAAGTATGGTAGTTACNCAAGTTANACATCTGT
ATGGAAAATACCACTTGGTTCTACAAATGNGG

30

Sequence ID - 663   nt: 627
GCCTCCCGGGTTCAGGGATTTCTCCTGCCTCAGCCTCCTGAGTGGCTGCATTGCAG
GCACCTGCCACCACGCCTTGCAAATTTTTGTGTTTTTAGTGGAGATGGGGTTTTGC
CATGTTGGCCAGGCTGGTCTCGGACTCCTGACCTCAGGTGATCCGCCCGCCTCAGC

35   CTCCCAGAGGGCTGGGATTACAGGCGTGAGCCACTGTGCCTGGCCCCAAGTTTTGC
ATCTTTTAATGCCCTCTGAACAAATACATAGAGAAAACTCTCAGAACAATTAAAAC
CTGCAGAGCAACAGTGTCCTCCATGTCTTAGGTTTCAAGTTTGCCTCTAAAATTCT

- 201 -

AATCCATATTTTTCTACTTCTCAGATAATTTATGTGTGTGTACTCTTCCTAGACGT
ACAAGAGACTTTTTAATGCTAAATATTTGTCAGTGCTTAACAAAAACTCAATTTCA
CATTACTCATATTGTTTTTGTTTTAATTGAATGTGAATTAAATTTTTATTAGTTAT
TTGATTTGGAATGTTATGTATGCCATTAACACTATTAGGGGAATCTCTAGCATTTC
5 TGTATTTTTAAAGAATTTGATTCTTTTGTANATTCTGCCTGTGTGGCATTTTAAAC
ATGTGTGACAT

Sequence ID - 665   nt: 345
ACCGGCGACATGGCCAAACGTACCAAGAAAGTCGGGATCGTCGGTAAATACGGGAC
10 CCGCTATGGGGCGTCCCTCCGGAAAATGGTGAAGAAAATTGAAATCAGCCAGCACG
CCAAGTACACTTGCTCTTTCTGTGGCAAAACCAAGATGAAGAGACGAGCTGTGGGG
ATCTGGCACTGTGGTTCCTGCATGAAGACAGTGGCTGGCGGTGCCTGGACGTACAA
TACCACTTCCGCTGTCACGGTAAAGTCCGCCATCAGAAGACTGAAGGAGTTGAAAG
ACCAGTAGACGCTCCTCTACTCTTTGAGACATCACTGGCCTATAATAAATGGGTTA
15 ATTTATGTA

Sequence ID - 666   nt: 252
ATAATTCAGAACTTCTTCATATGCTCGAGTCTCCAGAGTCACTCCGTTCTAAGGTT
GATGAAGCTGTAGCTGTACTACAAGCCCACCAAGCTAAAGAGGCTGCCCAGAAAGC
20 AGTTAACAGTGCCACCGGTGTTCCAACTGTTTAAAATTGATCAGGGACCATGAAAA
GAAACTTGTGCTTCACCGAAGAAAAATATCTAAACATCGAAAAACTTAAATATTAT
GGAAAAAAACATTGCAAAATATAAAAT

Sequence ID 669
25 TTACTTTTAACCAGNGAAATTGACCTGCCCGTGAANAGGCGGGCNTGACACAGCAA
GACGAGAAGACCCTATGGAGCTTTAATTTATTAATGCAAACGGTACCTAACAAACC
CACAGGTCCTAAACTACCAAACCTGCATTAAAAATTTCGGTTGGGGCGACCTCGGA
GCAGAACCCAACCTCCGAGCAGTACATGCTAAGACTTCACCAGTCAAAGCGAACTA
CTATACTCAATTGATCCAATAACTTGACCAACGGAACAAGTTACCCTAGGGATAAC
30 AGCGCAATCCTATT

Sequence ID 670
GGCTGATTCCTGAGCTATAAAAGCATAATTGCTTTATATTTTGGATCATTTTTTAC
TGGGGGCGGACTTGGGGGGGGTTGCATACAAAGATAACATATATATCCAACTTTCT
35 GAAATGAAATGTTTTTAGATTACTTTTTCAACTGTAAATAATGTACATTTAATGTC
ACAAGAAAAAAATGTCTTCTGCAAATTTTCTAGTATAACAGAAATTTTTGTAGATG
AAAAAAATCATTATGTTTAGAGGTCTAATGCTATGTTTTCATATTACAGAGTGAAT

TTGTATTTAAACAAAAATTTAAATTTTGGAATCCTCTAAACATTTTTGTATCTTTA
ATTGGTTTATTATTAAATAAATCATATAAAAATT

Sequence ID 671

CAGGAAGTCACCTGGGATTGGCTGCCTCACCCACTCACAGTGCCATCCCTGCCCCA
GGCCTCCCAGTGGCAATTCCAAACCTGGGTCCCTCCCTGAGCTCTCTGCCTTCTGC
TCTGTCTTTAATGCTACCAATGGGTATTGGGGATCGAGGGGTGATGTGTGGGTTAC
CTGAAAGAAACTACACCCTACCTCCACCACCTTACCCTCACCTGGAGAGCAGTTAT
TTCAGAACCATTCTACCTGGCATTTTATCTTATTTAGCTGACAGACCACCTCCACA
GTACATCCACCCTAACTCTATAAATGTTGATGGTAATACAGCATTATCTATCACCA
ATAACCCTTCAGCACTA

Sequence ID 672

CAGGAAGTCACCTGGGATTGGCTGCCTCACCCACTCACAGTGCCATCCCTGCCCCA
GGCCTCCCAGTGGCAATTCCAAACCTGGGTCCCTCCCTGAGCTCTCTGCCTTCTGC
TCTGTCTTTAATGCTACCAATGGGTATTGGGGATCGAGGGGTGATGTGTGGGTTAC
CTGAAAGAAACTACACCCTACCTCCACCACCTTACCCTCACCTGGAGAGCAGTTAT
TTCANAACCATTCTACCTGGCATTTTATCTTATTTAGCTGACAGACCACCTCCACA
GTACATCCACCCTAACTCTATAAATGTTGATGGTAATACAGCATTATCTATCACCA
ATAACCCTTCAGCACTAGATCCCTATCAGTCCAATGGAAATGTTGGATTANAACCA
GGCATTGTTTCAATANACTCTCGCTCTGTGAACACACATGG

Sequence ID 673

GGGTTTTCTTTCGGAAGCGCGCCTTGTGTTGGTACCCGGGAATTCGCGGCCGCGTC
GACTGCTAAACAGAATACTGCTATTTTGAGAGAGTCAAGACTCTTTCTTAAGGGCC
AAGAAAGCCACNTGNNCCCTNGGNCTAATCTGGCTGAGTAGTCAGTTATAAAAGCC
NTAATNGCTTNNTNTTTGGNNTCNTTTTTTNNCNGGGGNCGGNCTTGGGGGGGGTTG
CNTCCAAAGATANCATNTNTTTCCAACTTTNTNAANNNAANNGTTTTAAAATCCCT
TTTCCNCCNGAAAANANNGCCCTTTAAGNGCCNCAAAAAAAAANNGTNTTCTGCAN
NTTTTCTANTATNACAAANNTTTTNGTAGAANAAAAATTTTTTTTTAGNGGCTACC
CTTTNTTTNTTANNCANNGGAGTTTNTTTTTTACAAAAAAAAAAANATTGGGNCCCCT
CCACAACCTTGGGTCTNTAATNGGGGGGTTTTTAAATAAANCNTNTNTAAATCCCC
CNNNNNNNNNCNNNNNNNNNNCNNNNNNNNNNNNNNNCCCNNNNAAAAAATTTTTNC
TCCCCCNCCCTTTTTCTTCCTGCCGGCCCCAATTTAAGCCCNGGCGCTTGGGGCAA
ATCCCCCTTTAGNGGGGGGGGTTTANAAAAACCNGGGGCGGGGNTTTAAAACCNCGG
GGNNNGGGGAA

- 203 -

Sequence ID 674

ACCTCTAGCATCACCAGTATTAGAGGCACCGCCTGCCCAGTGACACATG-TTTAAC
GGCCGCGGTACCCTAACCGTGCAAAGGTAGCATAATCACTTGTTCCTTAATTAGGG
ACCTGTNTGAATGGCTCCACNAGGGTTCACTTGTCTCTTACTTTTAACCAGTGAAA
TTGACCTGCC

Sequence ID - 675   nt: 591

GTATAGAAAATAATGTCCCCAGNGCATAGAAAAAATGAGTCTCTGGGCCAGTGAAT
ACAAACATCATGTCGAGAATCATTGGAAGATATACAGAGTTCGTATTTCAGCTTT
GTTTATCCTTCCTGTTAAGAGCCTCTGAGTTTTTAGTTTTAAAAGGATGAAAAGCT
TATGCAACATGCTCAGCAGGAGCTTCATCAACGATATATGTCAGATCTAAAGGTAT
ATTTTCATTCTGTAATTATGTTACATAAAAGCAATGTAAATCAGAATAAATATGTT
AGACCAGAATAAAATTAATTATATTCTGGTCTTCAAAGGACACACAGAACAGATAT
CAGCAGAATCACTTAATACTTCATAGAACAAAAATCACTCAAAACCTGTTTATAAC
CAAAGAATTCATGAAAAGAAAGCCTTTGCCATTTGTCTTAGAAAGTTATTTTTTA
AAAAAAAATCATACTTACTATTAGTATCTATGGAAGTATATGTAACAATTTTTATG
TAAAGGTCATCTTTCTGTGATAGTGAAAAAATATGTCTTTACTAAGTTGAAATGAA
TACTTTCTGNCTTTGCTAATGGATAGTTATT

Sequence ID 676

CTCAATTCTACTAAAAAGCCCCCCAAGAAAAGCGAATGAGAAAACAGAGTCATCCT
CTGCACAGCAAGTAGCAGTGTCACGCCTTAGCGCTTCCAGCTCCAGCTCAGATTCC
AGCTCCTCCTCTTCCTCGTCGTCGTCTTCAGACACCAGTGATTCAGACTCAGGCTA
AGGGGTCAGGCCAGATGGGGCAGGAAGGCTNCGCAGGACCGGACCCCTAGACCACC
CTGCCCCACCTGCCCCTTCCCCCTTTGCTGTGACACTTCTTCATCTCACCCCCCCC
TGCCCCCCTCTAGGAGAGCTGGCTCTGCAGTGGGGGAGGGATGCAGGGA

Sequence ID 679

GNANCNTTTCCTNTCGNAAANCGCGCCTTGTGTTGGTACCCGGGAATTCGCGGCCG
CGTCGACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAANTNTAGACTCGANCAAGCTT
ATGCANGCNTGCGGCCGCAATTCGAGCTCGGCCGACTTGGCCAATTCGCCCTATAG
NGAGTCGTATTACAATTCACTGGCCGTCGTTTTACAACGTCGNGACTGGGAAAACC
CTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGT
AATANCGAANAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGG
CGAANGGAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTA
AATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAA
AAGAATAGACCGAGATAGGGTTGAGNGTTGTTCCAGTTTGGAACAANAGTCCACTN

TTAAAGAACGNGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGG
CCCACTACGTGAACCATCNCCCTAATCAAGTTTTTTGGGGTCGAGGNGCCGTAAAG
CACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAAAGCTTGACGGGGAAAGCCC
GGCGAACGTGGCGAAA

5

Sequence ID 682

CACCTGCAGTCCAAGTACATCGGCACGGGCCACGCCGACACCACCAAGTGGGAGTG
GCTGGTGAACCAACACCGCGACTCGTACTGCTCCTACATGGGCCACTTCGACCTTC
TCAACTACTTCGCCATTGCGGAGAATGAGAGCAAAGCGCGAGTCCGCTTCAACTTG
ATGGAAAAGATGCTTCAGCCTTGTGGACCGCCAGCCGACAAGCCCGAGGAAAACTG
AAACTTTGCTTAACNACCGAATGGNGGGGANCTTTTCCAACGNTTTT

10

Sequence ID 683

TTGGTTTCATACTGNTGGGGNTTGAATGNTCCCTNCAACACTNATGTTGANACTTA
ATCCCTAATGNGGCAATACTGAAAGGTGGGGCCTTTGAGATGTGATTGGATCGTAA
GGCTGTGCCTTCATTCATGGGTTAATGGATTAATGGGTTATCACAGGAATGGGACT
GGTGGCTTTATAAGAAGAGGAAAAGAGAACTGAGCTTGCATGCCC

15

Sequence ID - 684   nt: 545

GTGGAAGNGACATCGTCTTTAAACCCTGCGTGGCAATCCCTGACGCACCGCCGTGA
TGCCCANGGAAGACAGGGCGACCTGGAAGTCCAACTACTTCCTTAAGATCATCCAA
CTATTGGATGATTATCCGAAATGTTTCATTGTGGGAGCAGACAATGTGGGCTCCAA
GCAGATGCAGCAGATCCGCATGTCCCTTCNCGGGAAGGCTGTGGTGCTGATGGGCA
AGAACACCATGATGCGCAAGGCCATCCGAGGGCACCTGGAAAACAACCCAGCTCTG
GAGAAACTGCTGCCTCATATCCGGGGGAATGTGGGCTTTGTGTTCACCAAGGAGGA
CCTCACTGANATCAGGGACATGTTGCTGGCCAATAAGGTGCCAGCTGCTGCCCGTG
CTGGTGCCATTGCCCCATGTGAAGTCACTGTGCCAGCCCAGAACACTGGTCTCGGG
CCCGATAAGACCTCCTTTTTCCAGGCTTTAGGTATCACCACTAAAATCTCCAGGGG
CACCATTGAAATCCTGAGTGATGTGCACTGATCAAGACTGG

20

25

30

Sequence ID 685

GGAAAGGGCCATTTTATTGCCTAAAACCACCTGGNTTTTNAGGTAACAGTTCCAAC
ATGTCCTTTTTTGAATAGCTGTTCTAATTATTATATATTCAGCTGATTAATAGGAG
TACTTGATAGGTGGACTGTGTCAGGTAGCCTCAGGCAATCCTACTTCAACAAGCTG
TCAGGGAGCCATGCCATGCTTCTTTATGACATAGGTGAATTTGATAGGCTCACTAG
CAGAACATGGGATCACAAGGTGGAACCNTTCCNTTT

35

Sequence ID 686

GACCCCTTCCTTACACCTTATACAAAAAAACTGAAACTGGACCCCTTCCTTACACC
TTATACAAAAATTAACTCAATTTTATTATGTTGTATTAAATTAAGTTGGGTTTAAT
TAAGATGGATTAAAGACTTAATTATAAGACCTAAAACCATAAAAACCCTAGAAGAA
AACCTAGGCCATACCATTCAGGACACGGGTATGGGCAAAGACTTCATAACTAAAAC
ACCAAAAGCAATGGCAACGAAGTCCAAATAGACAAATTGGACCTGATTAAACTAAA
GAGCTTCAGCACAGCAGAAGAGACTATCGTCAGAGTGAACAGGCAACCCACAGAAT
GGAAGAAATTCTTGCAATCTATCCATCTGACAAGGGGCTAATATCCAAAATCTAC
AAAGAACTTAAACAAATTTACAAGGAAAAACACAAACAACCCCATCAAAAAGTGGG
CTAAGGATGTGAACAGACACTTCTCAAAAGAAACATTTATGCAGCCAACAAACAT
GAAAAAAGTTCATCATCACTGCTCATTAGAGACATGCAAATCAAAACCACAATGA
GATCCCATCCCACACCAGTTAGAATGGCAATCATTAAAAATGT

Sequence ID - 687   nt: 268

TTTATGTGTTTTTGCTTGGGGGGCGCTGGGCCTAGCCCAGAGTAGTGCTTGCTCCC
CCTGCCTTGTCCCACCAGGGAGGCAGCAGACTCAGGCCCTCCATGGTCCTCTTTGT
CATTTTGTTGACATGCATTCCTCCTTTTGTCATCTTGTTGGGGGGAGGGGATTAAC
CAAAGGCCACCCTGACTTTGTTTTTGTGGACACACAATAAAAGCCCCGTTTATTTG
TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

Sequence ID - 688   nt: 569

CTTTAGCCAGCCTGATCAGAAAAAAACAAAAGAAGAGGAAAGACGTAGATTACCAA
CATCAAGAATGTGAGTTATGATATCACTACAGACTCTCCAGGTATTAAAAGCATAA
TTAGAGAATGATATGAGCAGCTATATGCAAATAAGTTCAACATTGGACAAATGGAC
AAATTTCTTGAAAGATAAATTATGAAATTTCATTCTGAAAGAACTACATGACCTTA
ATTGTCTTACATCTATTAAATAAGTGGAAATTGTAGTTTAGAAACTTTCCCACAAA
GAAAACTCTAGGCCCAGATGGCATCAAAATAATATTCAGATGAATGAAATGGAGAA
AGGATAGCCTTTTCAACAAATGGTGGTGGAACAATTGGATTTCCATATGCAAAAAA
ATAGAGATGGACGCAGAGGTGTGTGCTTAGGAGGCTGAGGTGAGAGGATTGTTTGA
GGCCAGCCTGGGCAACATAGCAAGACCCCATTTCAAAAACAAAAATAAAGAACTTG
TAGCCTTACCTTGTGCCATATTATGAAAATGTATCATAGGCTTAAATGTGAAACGT
AAAACAAAA

Sequence ID 689

CGCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGTTT
TTTTCTCTTTGAAAGATAGAGATTAATACAACTACTTAAAAAATATAGTCAATAGG
TTACTAAGATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATT

TTAAGAGAAAATATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGG
TTTCTAAAACATGACGGAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTAT
TTAAAAGAAAATTGAGAGAAAGGACTACAGAGCCCCGAATTAATACTAATAGAAGG
GCAATGCTTTTAGATTAAAATGAAGGTGACTTAAACAGCTTAAAGTTTAGTTTAAA
AGTTGTAGGTGATTAAAATAATTTGAAGGCGATCTTTTAAAAAGAGATTAAACCGA
AGGTGATTAAAAGACCTTGAAATCCATGACGCAGGGAGAATTGC

Sequence ID 690

CGAAAAGCAAATATAACTTGCCACTAACCAAGATCACCTCTGCAAAAAGAAATGAA
AACAACTTTTGGÇAGGATTCTGTTTCATCTGACAGAATTCAGAAGCAGGAAAAAAA
GCCTTTTAAAAATACCGAGAACATTAAAAATTCGCATTTGAAGAAATCAGCATTTC
TAACTGAAGTGAGCCAAAAGGAAAATTATGCTGGGGCAAAGTTTAGTGATCCACCT
TCTCCTAGTGTTCTTCCAAAGCCTCCTAGTCACTGGATGGGAAGCACTGTTGAAAA
TTCCAACCAAAACAGGGAGCTGATGGCAGTACACTTAAAAACGCTCCTCAAAGTTC
AAACTTAGATTTCAGATTT

Sequence ID 691

CCGGTCTCTACACAATATATAGAAATCTGGGCATGGTGGTGCCTGGCTGTAGTCTC
AGCTACCTAGTTGGGTGAGGTGGGAGAGTCGCTTGAGTCCTGGAGGTTGAGGCTGT
AGTGAGCCAGGGCTGCACCACTGCATTCCAGCCTGGGTAACAGAGTGAGACCCTGT
CTCAAAAAGAAAAAAAAAAATTGCTAATTTTAACAAATCACAAAACTGACTCAGGC
AAGTTGTCTGACTCAAAAGCCCTTGAAAAACCATCAAAGACAGTAGAATGTTAACT
GGTCATTTACGTAAATAGTGTTCATTAAATTTTTGGTTCATTTAGGATAATCATT
TTAAATGAGACTGTATTTGAGACTGTATACACATACATATACATGTTTACACACAT
ATACGTACAATATATGTACATTCTATCTAAAAGATCATACATGTGTACATATAT
GTTTTTAAAAGTCAAACTGACATATTAATGGAAACAGTGCTTACATCTCTGGTAGT
GATTTTCTATTAGCAGCAGCCCTACATATGCTGCGTCTCTGAACAGCATGTCAGTG
CCATGACTGTCTAAACATGCAAATATGACTGACAGACTCTTGAGACAGCTTTCACC
TTG

Sequence ID 692

AATTCGNGGCCGCGTCNNCCTANGAGGCACCAGGAAATCCCGCGGGGTGGCCCATG
CAGACCAGGCGCACGTGGCTCATGGGGCANAATTGCCAAGGACAGCTCACGACAGT
GCCACCTTCTCACCATTCCAGCCAAGGAGAGATGTGACGTTGGAACTGCTCTGGCA
CTTCTGTCAAGCCTCCCCCGCCCCAATTGCCTTGAGATCTCTGCTCTTTGTCAGAG
ATTTGCAAAGACTCACGTTTTTGTTGTTTTCTCATCATTCCATTGTGATACTAAGA
AACTAAGAAGCTTAATGAAAGAAATAAAATGCCTATGTTGTTGTTCT

Sequence ID 693

CTAGAACCCATGACTCCTAGGTCTTATACTGCAACCACAGTATCAGCAAATAATCT
TTCATAAGGGGATTATTCTCTGATTAACAGGAAATACAGGAATTTAATTTGTGAAC
ACGCTAGGTAGAAGCAGAAACCCAAATCCAAATCCAAATTTAAACATTTAAAATTC
ATTCTATAACTAAGATCTAACAGTCATTTTCTTCCCAGTAAGAAATAACCAAAGCA
TGCTAAAAATCACTGGACTAAATTGGTGTCAAAACTGCCACATTGCCAGGCATGGG
GGGGTCATACTTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGAAAATTGCTTGA
GGCCAGGAGTTCGAAACCAGCCTGGGCAACACAGTGAGACCCCATCTCCACAAAAA
AAAAAATTAAAAAACAAAACAAAACATTAGCTGGGCATGGTGGTACACGCCTGTA
GTCCCAGCTACTCAGGAGCCTGAAGTGAGAGGATCACTGAAGCCCAGGAGGTAGAG
CTATGACTGTAGTGAGCTATGACTGTGCCACTACACTCCACCTGGGTGACAGGGGA
CTC

Sequence ID 694

CGACTTCCATTTGTATTAATGGAATACTAAGTCCCTCTGTGATTTCTGAACCAAGC
TATTCCTAGGCCTGAGTTTTATTTTGTTGACACAGAAATAAATTANAAGGCCAAGC
GTGGTGGCATGTGCCTGTAGTCCTAGTTGCTGAGGTAAGAGGATTGCTTGAGCCCA
GGAGTTCAAGGCTGCAGCAAGCTTTGATTGCGCCACTGCACTCCAGCCTTGGCGAC
AGACTAAGACGCTGTCTCAAAAAAAAACAAAAA

Sequence ID 696

GGTTATCAATGAGATTAAGAGACAACTAGAGTAAAAACAAAAGAAAAGAAAAGAAA
NGAAAACAACAGAAGCTCTATTAACTGACCTCTAACCAATACAACAGGTTAACTGA
TGTTCTCCATTCTGTATATAAAAATCCCAGTGGACACCCACAACACAGGCTTCAGG
CTTGTAGGACACTTTCTAGTTCATCTGAGCACTTTTGTTCTCAGCAGTTGAGCTGT
ATACTTAGCAACATTTGGTGCTTCCAAACCCATTTGTGCCTGTAGCACTTACTATT
GAAATACATAATTTAATTAAATATTATATAAAGGAATGGAATACGAGTTGGACAAG
AAAAAGAGTTAAATCTGAAGGTTAGGTAAAAGAGCAACTTCTTTTCTCTGTTTTG
CAGGTTGGCAAAATCATTTAAAAACAATTGGAAGTATTATATGTTCTGCATTAAGT
TGTCATTTTACTTAAAAACTAGGCATCAAAGATGATGCATAATAAATTTAGTGTAT
GCAAGAATGACTGCTTGGGACCTCAATATATGAATTCTTAATCCAAGGAAAGTCCT
TGGCCTTACATTTAAAAGTCGGCAAATAAGTGTACGTTCATT

Sequence ID 697.

GAACATTTAAAAATAATGCAAATAAGGCTGGGCGTGGGGGCTCACACCTGTAATCC
CAGCACTTTGGGAGGCCGAGGCAGGCAGATCACGAGGTCAGGAGATTGAGACCATC
CTGGCTAACACAGTGAAACCCTGTCTCTACTTAAAAAATAAAAAAATTAGCCAGGC

GTGGTGGTGGGCGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATGGT
GTGAACCCGGGAGGCGGAGCTTGCANTGAGCTGAGATCGTGCCACTGCACTCCAGC
CTGAGCGACAGAGCGAGACTCTGTCT

5   Sequence ID 698
TCATTAGAATCCAAGCTTTGAAAATTTCTGATTAATGCTCATGTATTTCTTTATCT
TTGTTTTTCCTTGTGAAGAAAGACTTTCACCACTGTCTGAGTGATGATGCTGTTGA
TAAGGATGATGTCGATGACTACTATATTGCATCTCTCAGGAACAGCTGATGGGAAG
GGAGGGGCTGCTGAGTTCCCTTGTTCTAGCTAGCAGCACGCTCCTCANAGAGGGGG
10   CCGAGTTACAGACAGCAGCCGCATTCTCATGCAAAATTAGTTTTAAACTGCTAGTG
TGGGCATCGGTACCTTTTGCCTGGGTGATACCGAAGAATTGTTGAGGATTTAGTAT
GCTCCGTAGAGACAGTTCAGCCAGTCATTTCTGCATTGGAGAGACTTCTCATACTT
TCTTTGAAGACTCATAGAAAGCTGGAT

15   Sequence ID 699
ATTAAGGTTTGTNCCCAACAAGAATAGATGTAATTAGAAAAAANTGNCTTCCTTAC
CTATTGCCTCTGATNTTTACTTGCTTAAATTTTTTTTATTGNAAATCCAGAAAAAG
NGGATTTAGAGAACAACACTAACTCCCACCTAATCTATGACAGANATGTACAANAN
AGTACCTGTGAAAAATGTGAAAGNATNTGAAAAATGTAACCTTTGGCAGCCTGAGC
20   ATAGTCAACCAGAAAAACTATCTGAATTAAAATAATTGGTCCATAGGTACTATTTT
ATTTGGTCCATAAGGATTATTTTTTCAACTTTTTTTTTCAAGTGTATTATTATGTCA
TTTCCCACGTAGGTTACTGATACCTGAAGACTTTTTNCACCTTTAACCTTNCTCGT
TGAGGAGCTTTGTANTCTAATAAAAGAGAAATATAAGTAAATGTTAGATATATGGG
NGGATAATGGTAACTATGTGCTTAAAGAGGTATAAAAGAAGGGTAGGGAGCAGATA
25   AGACAAAGGAAGGGCTATATTATAANGAAGAATATTCCAAGTAGGGAAGAGAAAAA
GATATGTTATCCATATAATATTTTATGTGCAGTAGAGAACATGTTCTATAGAANAG
ACAGAAGATG

Sequence ID 700
30   CTTGAGCCCAGGAATTCCAGCCTGGGCAATATAGTAAGACTCCGTCTCTACAAAAG
ATACAAAAATTAGCCAGATGTGGTGGTGCGTGCCTGTAGTTCCAGATACTGGAAAG
ACTGAGGCAGGAGGATTGCTTGAGCATGGGAAGTTGAGGCTGCAATGAGCTGTGAT
TACGCCACTACACTCCAGCCTGGGCAACAGAGTAAGATCTTGTCTCAAAAAAAAAA
TTGAATTCAGCTAAAAATAATAAAATTTTAAAATAATTTTAAAAAGCCCTCAACAG
35   CTTTGTTTTTCTCTCCTTGCCAGCTTCTCTGCAGCCTATAGCCTGCAGGCTGGCTG
CTGCGAGCCAGGACAAGCGGTGGGAAATGCAATCACAGCGTGAAATCTCTGTGTTC
AGAGACACGCAGGAAGCAGGTGAACCATGAAGGGCCAACACATGCCCCCAGTTAGC

- 209 -

AGGGTGTAGAGACCGGGGCAGGGCTTTCTTCTTCCTTCTGGGTTATAAATATCCAT
GTCCTGCCATTTGAAGCTGCAAGTGGCACACATGGATGCTGGACAGGCGCTCGCAC
TTTCTGGGCAGGGCANGGGGCTCAAAGGCAGGACAGCTGGGCAAAAGCACCTTGCG
TGGGCCC

5

Sequence ID - 701   nt: 579
CTTTGGAGCTTCTGTCTGTGCTGTGGACCTCAATGCAGATGGCTTCTCAGATCTGC
TCGTGGGAGCACCCATGCAGAGCACCATCAGAGAGGAAGGAAGAGTGTTTGTGTAC
ATCAACTCTGGCTCGGGAGCAGTAATGAATGCAATGGAAACAAACCTCGTTGGAAG
TGACAAATATGCTGCAAGATTTGGGGAATCTATAGTTAATCTTGGCGACATTGACA
ATGATGGCTTTGAAGGTAATTAAAATTATCAAATTGGTGCTTGATTTCTGCTTTTA
AAATGGTTTATGGAAGAAAATATGATTAAAGTTTTGTATTGTTTTCCTTCCTATAG
AAGATGGAGCCAGAATGGCATGCTAAGTTTTTTCTTTTCTTTAGTGTTATATATGA
CTTCTCCTCAATTGTCACCCATTGATCTTTACCACTGTTAATAATGGATGATATTC
AAAATACCTTATTTCAGTGATTCTAAGGCACCATTGATTAGAAACTGCATTATTAT
TTATGTGTCCCTAAAAGCTACCTATTAAGCTGTTACACCCACCATTTTTCTGTTAA
GAAAATCCTGATTTCAGAA

Sequence ID 702
GTNNTCCTCTCGGAACGCGCCTTNTGTAGCCAGGTGCTACCAGACCNAATACACGG
TTGTTCCAGCTTGCGCATTCACCGATGGCGTAGATATCCGGATCGGAAGTCTGGCA
GGAATCATTAATGACAATACCCCCACGCGGAGCAACGTCCAGACCACACTGGGTTG
CCAGCTTATCGCGCGGACGGATACCGGTAGAGAAGACGATAAAGTCGACTTCCAGT
TCGCTGCCGTCGGCAAAACGCATGGTTTTACGCGCTTCAACACCTTCCTGCACAAT
CTCAAGGGTGTTTTTGCTGGTGTGAACGCGCACGCCCATACTTTCGATTTTGCGAC
GCAGCTGCTCGCCGCCCATCTGATCAAGCTGTTCTGCCATCAGCATAGGGGCAAAT
TCGATAAC
GTGGGTTTCAATACCTAAGTTTTTCAGCGCGCCTGCGGCTTCCAGACCTAACAGGC
CGCAATTCGAGCTCGGCCGACTTGGCCAATTCGCCCTATAGTGAGTCGTATTACAA
TTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAAC
TTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGC
CCGCACCCGATCGCCCTTTCCAACAGTTGCGCACCTGAATGGCGAATGGAAATTGT
AAGCGTTAATATTTTGTTAAAATTCGCGT

Sequence ID 703
CTGCGCAGACCAGACTTCGCTCGTACTCGTGCGCCTCGCTTCGCTTTTCCTCCGCA
ACCATGTCTGACAAACCCGATATGGCTGAGATCGAGAAATTCGATAAGTCGAAACT

- 210 -

GAAGAAGACAGAGACGCAAGAGAAAAATCCACTGCCTTCCAAAGAAACGATTGAAC
AGGAGAAGCAAGCAGGCGAATCGTAATGAGGCGTGCGCCGCCAATATGCACTGTAC
ATTCCACAAGCATTGCCTTCTTATTTTACTTCTTTTAGCTGTTTAACTTTGTAAGA
TGCAAGAGGTTGGATCAAGTTTAAATGACTGTGCTGCCCCTTTCACATCAAAGAA

5   CTACTGACAACGAAGGCCGCGCCTGCCTTTCCCATCTGTCTATCTATCTGGCTGGC
AGGGAAGGAAAGAACTTGCATGTTGGTGAAGGAAGAAGTGGGGTGGAAGAAGTGGG
GGTGGGACGACAGTGAAATCTAA

Sequence ID 704

10   CTTGTATTCAAGAACTACTGTAATGCATTAGTGGTCTGGCTTCATTTTGTATGATG
CCAGATCCTTAATTTACCCAGCACAATCATTTCAGTAGTTTCCTATGGCTCCTGCA
AAAATGCAAACAGAAACCACCACAGGAACAGCCCCTTGCTGCCTCCTGTTGCTGAG
GTAGTAGTCGCTAAAGAAAATTGAAGGCTCCTTACAATCTATATTTGAAAACTAGA
ACTTCTGTAGAAACACACAGATCCCGATCTTAGAAGTTGTACAGGACAATCTGGTA

15   AAACTGACATAATTGTGATTTATTAACATGAATTAAAATGCCCAACCAGTGCTTCA
GTGTGACAGTATATTTAAAATAAAAAGAAATTAAAGGTCATATACTGTACTACTT
TCACAAGATCCACAGTTTTGCAAAAGACTTGTCATATGTACAATGCTATATATCA
AATGAGAAAAGCTGTAAGCAATTATATACGCAAAAGAAATGGCAGTA

20   Sequence ID 705

TTCCAGTCCTTTCATTTAGTATAAAAGAAATACTGAACAAGCCAGTGGGATGGAAT
TGAAAGAACTAATCATGAGGACTCTGTCCTGACACAGGTCCTCAAAGCTAGCAGAG
ATACGCAGACATTGTGGCATCTGGGTAGAAGAATACTGTATTGTGTGTGCAGTGCA
CAGTGTGTGGTGTGTGCACACTCATTCCTTCTGCTCTTGGGCACAGGCAGTGGGTG

25   TAGAGGTAACCAGTAGCTTTGAGAAGCTACATGTAGCTCACCAGTGGTTTTCTCTA
AGGAATCACAAAGGTAAACTACCCAACCACATGCCACGTAATATTTCAGCCATTCA
GAGGAAACTGTTTTCTCTTTATTTGCTTATATGTTAATATGGTTTTTAAATTGGTA
ACTTTTATATAGTATGGTAACAGTATGTTAATACACACATACATATGCACACATGC
TTTGGGTCCTTCCATAATACTTTTATATTTGTAAATCAATGTTTTTGGAGCAATCC

30   CAAGTTTAAGGGAAATATTTTTGTAAA

Sequence ID - 706   nt: 496
CAACCCTCTCTCCTCAGCGCTTCTTCTTTCTTGGTTTGATCCTGACTGCTGTCATG
GCGTGCCCTCTGGAGAAGGCCCTGGATGTGATGGTGTCCACCTTCCACAAGTACTC

35   GGGCAAAGAGGGTGACAAGTTCAAGCTCAACAAGTCAGAACTAAAGGAGCTGCTGA
CCCGGGAGCTGCCCAGCTTCTTGGGGAAAAGGACAGATGAAGCTGCTTTCCAGAAG
CTGATGAGCAACTTGGACAGCAACAGGGACAACGAGGTGGACTTCCAAGAGTACTG

- 211 -

TGTCTTCCTGTCCTGCATCGCCATGATGTGTAACGAATTCTTTGAAGGCTTCCCAG
ATAAGCAGCCCAGGAAGAAATGAAAACTCCTCTGATGTGGTTGGGGGGTCTGCCAG
CTGGGGCCCTCCCTGTCGCCAGTGGGCACTTTTTTTTTTCCACCCTGGCTCCTTCA
ACACGTGCTTGATGCTGAGCAAAGTTCAATAAAGATTTTGGGAAGTTT

5

Sequence ID - 707   nt: 397
CGGATGTGGTGGCAGGCGCCTCTAGTCCCAGCTACTCGGCAGGCTGAGGTAGGAGA
ATGGCTTGAACCCAGGAGGTGGAGCTGACAGTGAGCCGAGATCGCGCCACTGCACT
CCAGCCTGGGCGGCAGAGCGAGACTCCATCTCAAAAAAAAAAAAAAAAAAATAGA
CTTTGAGACCAGCCTGACCAACATAGTGAAACCCGTCACTACTAAAAATACAAAAA
TTACCCGGGCGTGGTGACGGGCGCCTGTAATCCCAGCTACTTGGGAGGCTGAGACA
GGAGAATCACTTGAACCAGGGAGGCGGAGGTTGTAGTGAACTGAAATCGTGCCCCT
GCACTCCAGCCTGGGTAACAAGAGCGAAACTCCGTCTCAAAAATAAATAAATAAAT
AAAAT

15

Sequence ID - 708   nt: 293
CCAGCTTTTTATGGTGTTTAATCTAATACACTTAAGCTGCAGTCCCAAAATTAGGG
GTCCTTCAGTCTTGGAGACTATAAGGGAGCCTCTGCACCCAGGGAAAATGTTACCC
TTTACAGGGGGGAAGGGTAAACCAGTAGGGAATACAGTACAATCCCAACCCTACTG
GGAGGGGCGGGAGGGAGGTGTTGCCGTCACTGTATTAAGTCGATGTTGGGAAACGT
TTTAACATCTGGAGCCTTTGTGGGTGGAAATATGTCTCCAGTTACAACTCCGCAGT
GGATGTGAAGAAG

Sequence ID 709
GGAAGCTACAATGATTTTGGGAATTACAACAATCAGTCTTCAAATTTTGGACCCAT
GAAGGGAGGAAATTTTGGAGGCAGAAGCTCTGGCCCCTATGGCGGTGGAGGCCAAT
ACTTTGCAAAACCACGAAACCAAGGTGGCTATGGCGGTTCCAGCAGCAGCAGTAGC
TATGGCAGTGGCAGAAGATTTTAATTAGGAAACAAAGCTTANCAGGAGAGGAGAGC
CAGAGAAGTGACAGGGAAGCTACAGGTTACAACAGATTTGTGAACTCAGCCAAGCA
CAGTGGTGGCAGGGCCTAGCTGCTACAAAGAAGACATGTTTTAGACAAATACTCAT
GTGTATGGGCAAAAAACTCGAGGACTGTATTTGTGACTAATTGTATAACAGGTTAT
TTTAGTTTCTGTTCTGTGGAAAGTGTAAAGCATTCCAACAAAGGGGTTTTAATGTA
NATT

Sequence ID 710
TGGATTCCCGTCGTAACTTAAAGGGAAACTTTCACAATGTCCGGAGCCCTTGATGT
CCTGCAAATGAAGGAGGAGGATGTCCTTAAGTTCCTTGCAGCAGGAACCCACTTAG

- 212 -

GTGGCACCAATCTTGACTTCCAGATGGAACAGTACATCTATAAAAGGAAAAGTGAT
GGCATCTATATCATAAATCTCAAGAGGACCTGGGAGAAGCTTCTGCTGGCAGCTCG
TGCAATTGTTGCCATTGAAAACCCTGCTGATGTCAGTGTTATATCCTCCAGGAATA
CTGGCCAGAGGGCTGTGCTGAAGTTTGCTGCTGCCACTGGAGCCACTCCAATTGCT
GGCCGCTTCACTCCTGGAACCTTCACTAACCAGATCCAGGCAGCCTTCCGGGAGCC
ACGGCTTCTTGTGGTTACTGACCCCAGGGCTGACCACCAGCCTCTCACGGAGGCAT
CTTATGTTAACCTACCTACCATTGCCCTGTGT

Sequence ID - 711   nt: 498
GTGGTACATATACACAAAGGAAAACTATGTAGCCATTAAAAGAAAAGGAACTCCTA
TCATTTGTAACAACATAAATAAATCTGGAGGAGATTAGGCTAAGGTGAAATAAGCC
AGGCACAAAAAGACAACTACCATGATCTTACTTATACGTGTGTGGAATCTAAAA
AGGTGGAATTTACAGAAGCAGAGAGTAGAATGGTGATTACCAGAGGCTGGGGAGTG
AGGGCAGGAGGTTGGAGAAATGTTGGTCAAAGGATACAAAGTTTCAGTTATACAGG
ATGAATAAGTTCAAGAGATCTATTGTACAACGTGGTGGCTATAGTTGATAACAATG
TATTGTGTTCTTGAAAAATGCTGAGAGAGTAGATTTTAAGTGTTCTCACCACAAAA
CATAAGTATGTGAGGTAATGCATGTGTTAATTANCTTAATTTAGACATTTCATAAT
GTATTATACATATTTCAAAACCACGTTGTACATGAGAAAGATACACAATT

Sequence ID 713
GCCCAGTCGACCCATGTTCTCCTTTCTACACCAGCATTAGACGCTGTCTTCACAGA
TTTGGAAATCCTGGCTGCCATTTTTGCAGCTGCCATCCATGACGTTGATCATCCTG
GAGTCTCCAATCAGTTTCTCATCAACACAAATTCAGAACTTGCTTTGATGTATAAT
GATGAATCTGTGTTGGAAAATCATCACCTTGCTGTGGGTTTCAAACTGCTGCAAGA
AGAACACTGTGACATCTTCATGAATCTCACCAAGAAGCAGCGTCAGACACTCAGGA
AGATGGTTATTGACATGGTGTTAGCAACTGATATGTCTAAACATATGAGCCTGCTG
GCAGACCTGAAGACAATGGTAGAAACGAAGAAAGTTACAAGTTCAGGCGTTCTTCT
CCTAGACAACTATACCCGATCGCATTCAGGTCCTTCGCAACATGGTCACTGTGCAG
ACCTGAGCAACCCCACCAAGTCCTTG

Sequence ID 714
CTGTAACAGAGATTCCTTTTTTCAATAATCTTAATTCAAAAGCATTATTAGACTTG
AAAGGGTTTGATAATCTCCCAGTCCTTAGTAAAGATTGAGAGAGGCTGGAGCAGTT
TTCAGTTTTAAATGAGTCTGCAGTTAATATCAAATGTGAGTTTGGGACTGCCTGGC
AACATTTATATTTCTTATTCAGAACCCTTGATGAGACTATTTTTAAACATACTAGT
CTGCTGATAGAAAGCACTATACATCCTATTGTTTCTTTCTTTCCAAAATCAGCCTT
CTGTCTGTAACAAAAATGTACTTTATAGAGATGGAGGAAAAGGTCTAATACTACAT

- 213 -

AGCCTTAAGTGTTTCTGTCATTGTTCAAGTGTATTTTCTGTAACAGAAACATATTT
GGAATGTTTTTCTTTTCCCCTTATAAATTGTAATTCCTGAAATACTGCTGCTTTAA
AAAGTCCCACTGTCAGATTATATTATCTAACAATTGAATATTGNAAATATACTTGG
CTTACCTCTCAATAAAAGGGTCTTTTCTATT

5

Sequence ID 717

TCCACCCACCTTGACCTCCCAAAGTGCTGGGATTATAGGCGTGAGCCACCTCGCCC
AGCCCGATACTAGGACTTATGCAGAAAAAACCTTGACATGGAGGAAAGTAAGATCT
AAATAAATACTGTATTCATAGATTAAAAGACTCAGCATAATAAATATACCATTTCT
CCCCAGATTGATGTACAGATTTAACACAATTCCTATCAAGATCCCAGCAAGATTTT
TGTAGATATGTAAAGATTATTCAAAAATGTAAAAGGAAGGACAAAGGACTAGAAT
AGATAAACAAAATGGAGAAAGATTTAATAGGAATCACTGTAACTGATTTTAAGAC
ATACAGAACAATAATAGAAACTGCTTGTATTAGTCCATTTTCACGCTGCTGATAAA
GACATACCTGAGATTGGCAATTACAAAGGAAAGANGTTTATTGGCTTACAGTTCCC

15   ATGGCTGGGGAGGCCT

Sequence ID 718

CTCCTCTGGGTTGAAACCCGGGCGCCGCCAAGATGCCGGCTTACCACTCTTCTCTC
ATGGATCCTGATACCAAACTCATCGGAAACATGGCACTGTTGCCTATCAGAAGTCA

20   ATTCAAAGGACCTGCCCCCAGAGAGACAAAAGATACAGATATTGTGGATGAAGCCA
TCTATTACTTCAAGGCCAATGTCTTCTTCAAAAACTATGAAATTAAGAATGAAGCT
GATAGGACCTTGATATATATAACTCTCTACATTTCTGAATGTCTGAAGAAACTGCA
AAAGTGCAATTCCAAAAGCCAAGGTGAGAAAGAAATGTATACGCTGGGAATCACTA
ATTTTCCCATTCCTGGAGAGCCTGGTTTTCCACTTAACGCAATTTATGCCAAACCT

25   GCAAACAAACAGGAAGATGAAGTGATGAGAGCCTATTTACAACAGCTAAGGCAAGA
GACTGGACTGAGACTTTGTGAGAAAGTTTTCGACCCTCAGAATGATAAACCCAGC
AAGTGGNGGGCTTGCTTTGTGAAGAGACAGTTCATGAACAANAGTCTTTCAGGACC
TGGACAGTGAAGGGAGCCCGGGCAGCCA

30   Sequence ID 719

CGNGGCCGCGTNAACTTTTGATCGTCAGCTGGGGCTGGCAGGCACCTAAATGGGAA
GGGTGATAGCAGTGTGTTGGGGGGAGTTTAGGGAACGGTCCTCTACCGATAGAGGC
AGCANCTCATTGGAATTTCCTCCTGAAGTTGTCTTGCCCCTTGAATCCTGCAGGAA
GGCTGGCAAATGGCCATTTCCCTTCCACTTGAATAGAGACCCATAACTCAAGTATC

35   TGCCCTTAAGACACCACAGGACTGTTCTTCGCGGGCCCTGCCCCTGGATTTGGGAG
AGGCAGTCCANCTCACCCAACTAGGCTCTGCANGGGGACCANGAGGGATGGGTTGT
GTCCACAGGACCAGCCAGACTGATGAGGGATGCGGCAAGCATATTCTCACCACCTT

- 214 -

CTTTCACGTTTACAACANACCAGCNTTCCCTGTGTGGCAGGGGTTACATTGGTCAC
CGAGGACCTANAATCATGGAGTGCTCTGGGGATCCGGGCTTGGA

Sequence ID 720

TCAGTGTTGAATTTTGTCAGACACTTTCTCTGCATCAATTGGTATGACCATGTGAT
TTTTTTTCTGTAGCCTGTTAATATGGTTAATTTTCAAATATTGAGCTGATTAATTT
TCAAATATTGAGCTCTCCTTGCATCTCTGGAATAAGTACCACTTGGTCGTGGTATA
TATTTCTTTTAATATATTGCTGAATTCTGTTTGATCATGTTTTCTTAAAGACTTTC
GTGTCTGTTTTCATGATAGATACTGGTCTATAGTTTTGTTGTAATATCTTGGTTTG
ATTTTGATATCAGGATAATGCTACCTTAATAGAATGAATTGGAGCCAAGTATGGTG
GCAAATGCCTATAGTCCTAGCTACTCAGGAGGCTGAGGTGGTGGGGACTGCTTGAC
CCANGAGTTCAAATCTAGCTTGGGCAATGTAGCAAGAC

Sequence ID 721

TAGAAGGAATGACTATTCATGTCCAAAGTGAATGGTTTTGTGCAGTGAACAACACA
TGGCGAGGTACTAACTGAGAAACTTTTTCATGCTTTATGCCTACCTCTTGTAGTTG
TTGCAGAGCAAATATAAATTGTAATAAGATAGCTAGGCCTTGCAGAAACAAACAGA
AAAACTTAAAAAAAAATGATATAAGAGCTGGAGTCTAGTATTTATATGAATCTGTG
AGAGATAATTTTTTTGGTCTCACTGCAATGAACCAAAAGCGGCTGAGTTTGGTTTT
TAATTGTAGCCATGTATTGAAGGCATCTTTTTGACCAACTCTTGTTGGTTCTGTCT
TGAACCATTGTTAATCACTGTGCTGTAATTAGTATAGCTAAATCTTTTCCTTCCTT
GCTCCTCCCCCAGCCCACCCCGTCTTCCCTTAACATTTTTTCAGGGGGGGTTGGGA
GTGGTTTCATTTTAATGTGAGTGGATGTTTTGATAGTTGTAAGGAAAAAATGCATT
TCAGACACATTTCACACATGAGCTATTTTCTTACACAGTATGTCTTATTGGTAATA
AGAATGTAATTCAT

Sequence ID 722

CNTTCCNTAAGAATACAAAAAATTAGCTGGGCGTGGTGGCAGGCGCCTGTAATCCC
ATCTACTCAGGAAGCTGAGGCTGGAGAATCGCTTGAACCCGGGAGGCGGAGGTTGC
AGTGAGCAGAGATCACGCCACTGCAGTCCAGCCTGGGCAACAGTGCGAGACTCTGT
CTCAAAAAAAAAATAAATAAATTACCTGGGTGTGGCAGCGCGTGCCTGTAATCCCA
GCTACCCAGGAGGCTGAGGCAAGAGAACTGCTTGAACCCAGGAGGCAGAGGTTGCA
TGGAGCTGAGATGGCGCCACTGCACTCCAGTCTGGTGACAGAGTGAG

Sequence ID 724

CTCTCTACTAAAAATACAAAAATTAGCTGGGCACGGNGGTGCATGCCTGTAAACCC
AGCTACCAGGTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCAGGGAGTCGG

- 215 -

AGGTTGCGGCGAGCTGAGATCATGCCACTGCACTGCGGCCTGGAGACAAGAGCAAG
ACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGACNTCACCTAATTGCAG
NGNGNGGACCTTATTTGGCTNTTAATTCAAACTATTAAAAATGTGAACN

5   Sequence ID - 726   nt: 260
     CGGGGTCTGTACCGGGCTGGCCTGTGCCTATCACCTCTTATGCACACCTCCCACCC
     CCTGTATTCCCACCCCTGGACTGGTGGCCCCTGCCTTGGGGAAGGTCTCCCCATGT
     GCCTGCACCAGGAGACAGACAGAGAAGGCAGCAGGCGGCCTTTGTTGCTCAGCAAG
     GGGCTCTGCCCTCCCTCCTTCCTTCTTGCTTCTCATAGCCCCGGTGTGCGGTGCAT
10   ACACCCCCACCTCCTGCAATAAATAGTAGCATCGG

     Sequence ID 727
     CTGAGTNTAGAAATGATGCCATTAATACTGATTGCAAAAACATTACAACTCAGTAC
     TGCAGCTTTCATTCAAATAGGTTATATGTATAAACTGAGTTCAACAATATTGTATT
15   TGAGATGGTAAAGTTAAAGAAATGCAATAATGTAAATAATACTTAAGAAAATAAGA
     TCTCAGGAAACTGTATATACTCTGTACTTTTATGCAACTTTATCAGATCATTTCAG
     TATATGCATCAAGGATATAGTGTATATGACATGAACTTTGAGTGCAAAAACTGTAC
     TATGTACCTTTTGTTTATTTTGCTGTCAACATCTAAATAAAGGTTTTTTTGTTTGT
     TTTTGTTTTTTTAATTGTTTTGTTTTAAAGATTGTTTTAATTAATTAAAAAATTA
20   ATTGTTTTAATTAAACAATTGTTTAATTGTTTTAAAGTCGCCAGGCTGAGGCAGGT
     GAATCACAAGCTTAGGAGTTGGAGGCTAGCCTGCCAACATGGTGAAACCCCGTCTC
     TACTAAAAATACAAAAAATTAACTGGGTGTGGG

     Sequence ID 728
25   CCCATCTGCACCAGTACACAGGCAGGCATTATCATTCTTCACCTACTTTTTAAATA
     GTGGCAACTTGGGATTCATTCTGGTGATTCTGAACCTTGCCTCATAGCTTAAAGTA
     TAAAAAGATTCAAGAGCAGTGAGGTTTGTTCTTTCCAGTGAATGGTGGACTGAGT
     GGTGCGAGGTGGAGGGCTAACAAGAGGAAAGAACTACATTCTTCAGAATACAGTGA
     TGAAAATTCATTTTGAAACTCAAATATTTTCATTTTGGATATTCTCCTGTTTTTAT
30   TAAACCAGTGATTACACCTGGCCATCCCTCTAAATGTTCTAGGAAGGCATGTCTAT
     TGTGATTTTGATGAAGACAGAATTATTTTTCTCTGTAGAAACACAGATACCACTTT
     ATCAGGGGAAGTTAGTCAAATGAAATGGAAATTGGTAAATGGACAAAAGCTAGCTA
     GTAAAAAGGACGACCCAGCAACATGCTTTAACCCCATTGTATGTTTGTGGAAAGAG
     CATAGTTTAACATCTTGAGAAATTTGGGACATAAAAGTTTTCATNGGTAGACAGTT
35   CATGGCAGTATATGAATTGACATAATGGAAATAATCTGATTTTATTTTTACAACTA
     ACATCCTTTCCCC

Sequence ID - 736   nt: 641

GGAATTCCAAGTGCTTGGGGATAATGATACCTCTGACCTTTCTTCCTTTTGGGAAG
TACTTGAGTGTGCAGCTGCATGAGGCCTCAGCAGGAGAGAGATTTTAGGTCCAAGA
AGCTATACCAGTAGGACAAGGCAGGAAAATACTACACTTTCAGGATCAAGCCCCTC
TGACTCTCATTTGGAAACTGGATGTTTGCTAAGCACCTGCTTCTTAAGGATGCCGA
GGGATTTAATGATACTCCCAGAAACCTGGAGAGATTAATGGGGCCTATGGAGAAGT
GCTCTGAACTCAGTGTTGGGACTTGAATAAAATTAACCATTGTCATGTTTTCAGAA
CAACTAAGCTGTTTTATATTTCATGTGCATGAAAGCCCTAGAACTAAGTTGTGTTA
TTTCCAGAAATGAAATAGATCCCACAGTTAGATGATGTGGCCATTAGGAAGTACCA
AATTTATAAAATCACTGGAGGTCTGTCTGAGCAGTACCTAATAAAATATAGTATA
CTGAAAGTGAACAGATACTTTGTCTCTTTCTTTGGCTGCTTGATCTTTATCTGTGT
CTGCCGTACAGTGCACCCTTAAAGTATTCTACACCAGTGCTTCTCAAACTGGAAAT
GTGCATGTAAGTCACCCANGGGTCT

Sequence ID 739

TGCATGCCCATAGTCCCAGCTATTTGGGAGGCTGAGGCAGGAAAATCGCTTGAACC
CGGGAGCCAGAGGTTGCAGTGAGCCGAGATCGCACTCCAGCTTGGCGACAGAACAA
GACTCTGTCTCAAAAAAAAAAAAAAAAGAAATCTTGGGATCCTGAACCCCTTACTC
GAAGGGCTAAGGTAGCATCTCAGCATGTCTTATTCGAGACTTCGTANAACCAGACC
TGCTGTTTGTAGATGTTAATTAATCAAACCTTTCTCTACTCATTCTGGACCAGTTA
AGGTTTTCTCCTTCTCCGTATGAGTTTTGATTTTCGTCCTCCTTGGTTGGAGATCA
CACTTTGGTCTGCTGCTAAGTTGGATGCCTCCCACTGTCTTTCCCTAAGTCTAGGG
CTTCANACCCCAGTGTGGGGAGAGGGACTTTCGTTTCCTGCCCCTCACCACATCAG
ACACAGGCAGGCAAGAATAAGATGGCCAAAAGGCCGATGAACTTCTTGACCTAGCC
TGGGACATTACCTGTTACTAGGTGGACTTCACTGCCTGTGAATGGAAGCTGAAGGG
CTGTTTTTTTGGTTTGTATTTGGACAGGCCAGGCTTANAGAGGGAGAGAACTGGGC
TACTCTTCAGCAGTGATCTTTAAAATGCC

Sequence ID 747

CAGAGTGCAAGACGATGACTTGCAAAATGTCGCAGCTGGAACGCAACATAGAGACC
ATCATCAACACCTTCCACCAATACTCTGTGAAGCTGGGGCACCCAGACACCCTGAA
CCAGGGGGAATTCAAAGAGCTGGTGCGAAAGATCTGCAAAATTTTCTCAAGAAGG
AGAATAAGAATGAAAAGGTCATAGAACACATCATGGAGGACCTGGACACAAATGCA
GACAAGCAGCTGAGCTTCGAGGAGTTCATCATGCTGATGGCGAGGCTAACCTGGGC
CTCCCACGAGAAGATGCACGAGGGTGACGAGGGCCCTGGCCACCACCATAAGCCAG
GCCTCGGGGAGGGCACCCCCTAAGACCACAGTGGCCAAGATCACAGTGGCCACGGC

- 217 -

CACGGCCACAGTCATGGTGGCCACGGCCACAGCCACTAATCAGGAGGCCAGGCCAC
CCTGCCTCTACCCAACCAGGGCCCCGGGGCCTGTTATGTCAAACTGTCTTGGCTGT
GGGGCTAGGGGCTGGGGCCAAATAAAGTCTCTTTCCTC

5   Sequence ID - 757   nt: 583
GAACCCTGCGGAGGGACTTCAATCACATCAATGTAGAACTCAGCCTTCTTGGAAAG
AAAAAAAAGAGGCTCCGGGTTGACAAATGGTGGGGTAACAGAAAGGAACTGGCTAC
CGTTCGGACTATTTGTAGTCATGTACAGAACATGATCAAGGGTGTTACACTGGGCT
TCCGTTACAAGATGAGGTCTGTGTATGCTCACTTCCCCATCAACGTTGTTATCCAG
10   GAGAATGGGTCTCTTGTTGAAATCCGAAATTTCTTGGGTGAAAAATACATCCGCAG
GGTTCGGATGAGACCAGGTGTTGCTTGTTCAGTATCTCAAGCCCAGAAAGATGAAT
TAATCCTTGAAGGAAATGACATTGAGCTTGTTTCAAATTCAGCGGCTTTGATTCAG
CAAGCCACAACAGTTAAAAACAAGGATATCAGGAAATTTTTGGATGGTATCTATGT
CTCTGAAAAAGGAACTGTTCAGCAGGCTGATGAATAAGATCTAAGAGTTACCTGGC
15   TACAGAAAGAAGATGCCAGATGACACTTAAGACCTACTTGTGATATTTAAATGATG
CAATAAAAGACCTATTGATTTGG

         Sequence ID - 758   nt: 424
         CTTGGCTCCTGTGGAGGCCTGCTGGGAACGGGACTTCTAAAAGGAACTATGTCTGG
20   AAGGCTGTGGTCCAAGGCCATTTTTGCTGGCTATAAGCGGGGTCTCCGGAACCAAA
GGGAGCACACAGCTCTTCTTAAAATTGAAGGTGTTTACGCCCGAGATGAAACAGAA
TTCTATTTGGGCAAGAGATGCGCTTATGTATATAAAGCAAAGAACAACACAGTCAC
TCCTGGCGGCAAACCAAACAAAACCAGAGTCATCTGGGGAAAAGTAACTCGGGCCC
ATGGAAACAGTGGCATGGTTCGTGCCAAATTCCGAAGCAATCTTCCTGCTAAGGCC
25   ATTGGACACAGAATCCGAGTGATGCTGTACCCCTCAAGGATTTAAACTAACGAAAA
ATCAATAAATAAATGTGGATTTGTGCTCTTGT

         Sequence ID - 764   nt: 626
         GATTTTTTTTTTTTTTTGAGATGGAGTCTTTCTCTGTCGCCCAGGCTGGAGTGCA
30   GTGGTGAAATCTCGACTCACTGCAACCTCCGTCTCCTGGGTTCAAGCAATTCTCCT
GCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACCAGCCACCACGCCCGGCTAAT
TTTTGTATTTTTAGTAGAGACAGGTTTTCACCATGTTGGCTAGGCTGATTTTGAAC
TCATGACCCCAAGTGATCTGCCCGCCTCGGCCTCCCAAAGTGCTGGAATTACAGGT
GTGAGCTACCACTCCCAGCCAATGATTACATTTATAAGGTAAAATAACTTGTGCCA
35   ATCTGTACAAGTGAATTCAGATTTAAAATTTTAATTGTAAAAGATATCCAGGTGA
TATTTCTCCTGAATAATTTAGTTTCCTTTTCTATTTCTTGATATAAAAGTACTCA
GCATTGAAGTAATTGCTATCTTCACATTTCTTCCTATTTGAGCTGTCTAAATAAGT

- 218 -

AGTCCTACATATTTTCCCCCCAACACAAAAAAACCCAGAAAAGAATTATTTTATACT
GGATTTTTTTGGTTGTAGCAGGAACCTAAAGGNGCCAATTGTAACATGCATGTTCT
TTTTGGCAAA

5   Sequence ID 766

GTCCATCCTGCAGGCCACAAGCTCTGGATGAGGAACTTGAGGCAAGTCACCAGCCC
CTGATCATTTCGCCTAAAAGAGCAAGGACTAGAGTTCCTGACCTCCAGGCCAGTCC
CTGATCCCTGACCTAATGTTATCGCGGAATGATGATATATGTATCTACGGGGGCCT
GGGGCTGGGCGGGCTCCTGCTTCTGGCAGTGGTCCTTCTGTCCGCCTGCCTGTGTT
10   GGCTGCATCGAAGAGTAAAGAGGCTGGAGAGGAGCTGGGCCCAGGGCTCCTCAGAG
CAGGAACTCCACTATGCATCTCTGCAGAGGCTGCCAGTGCCCAGCAGTGAGGGACC
TGACCTCAGGGGCAGAGACAAGAGAGGCACCAAGGAGGATCCAAGAGCTGACTATG
CCTGCATTGCTGAGAACAAACCCACCTGAGCACCCCAGACACCTTCCTCAACCCAG
GCGGGTGGACAGGGTCCCCCTGTGGTCCAGCCAGTAAAAACCATGGTCCCCCCACT
15   TCTGTGTCTCAGTCCTCTCAGTCATCTCGAGCCTCCGTTCAAAATGATCATCATCA
AAACTTATGTGGCTTTTTGACCTTTGAATAGGGAATTTTTTAAAATTTTTTAAAAA
TT

Sequence ID 768

20   CCAGCGCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAA
GTTTTTTTCTCTTTGAAAGATAGAGATTAATACAACTACTTAAAAAATATAGTCAA
TAGGTTACTAAGATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAA
GATTTTAAGAGAAAATATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAA
AAGGTTTCTAAAACATGACGGAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAAT
25   GTATTTAAAAGAAAATTGAGAGAAAGGACTACAGAGCCCCGAATTAATACCAATAG
AAGGGCAATGCTTTTAGATTAAAATGAAGGTGACTTAAACAGCTTAAAGTTTAGTT
TAAAAGTTGTAGGTGATTAAAATAATTTGAAGGCGATCTTTTAAAAAGAGATTAAA
CCGAAGGTGATTAAAAGACCTTGAAATCCATGACGCAGGGAGAATTGCGTCATTTA
AAGCCTAGTTAACGCATTTACTAAACGCAGACGAAAATGGAAAGATTAATTGGGAG
30   TGGTAGGATGAAACAATTTGGAGAAGATAGAAGTTT

Sequence ID 773

GAGGAAAGGGGAGTTAATATTTAGTGGACAGAATTTCAGTTTTACAGATGAAAAGA
GTTCTGGAGATAGACGGTGTTGATAGTTGCACAGCAGTGTGAATGTGCTCATTGTT
35   ACCGAACTTAAAAATGTTTAACATAGTATTATGTGATTTTTATTTTGCCACTTAAA
AAAAAGAATGAAGTACTGATACATGCTACAACATGGGTGAGCTTTAAATACATTC
TGCTCAGTGAAATAAGCCAGATGCAAAGATCACATATTATATAATCCACTTATAC

- 219 -

GAGATACCTAGAATAGGCAAATTCATAGAGACAGAAAGTAGAATAGTGGTTCCCAG
GGGCTGGGGACAAGGGGGCAGTGAGAGATTGAGAGTTATTATTAATGCGTACAGAG
TTTCAGTTTGGGCTGATAAAAAAGTTCTGAAGATGGATGGTGATGATGGTTGTACA
TCAATGTGAGTGTAATTACCGCCACTGAACTGCCCTTAAAAACGTTTAAAAGAGTA
AATTTTATGTTGNGTATATTTTACCATAAT

Sequence ID 776

TTTTTTTTTCATAAGAGGCAAGTACAAGAAAAAGCTTAATTACTTTAACTTCTAAG
TAGTTTGGAATCTAAATAAATAGGAGTTACCAAATATATGCGCTTCTGTGAATAGT
TTTCCCCCACATGTTTATTTATATTTTTGCATCTCATCAAACCTAACAGATTCTAA
AGTCTCTGGTGATAATGACAATATCTGCTACGGAGAGACTAGCCTGGGGGAAGAGG
ATCTCCCTGAACAAGGATAGCGGAGTTGCTGCAGCTTTCAAATGAAGCTGGACATT
TAGCTGCGGGGGTAGCACCCTTTGATCAAGGCAGCCCAAAGATGAGTTTCAGGGAT
GGGACTGACAGAAGAGAAAAGTTCTTCCCAGCCCTTTCTACTTTTTCTCTTTGTTT
CTCAGGCTTCTGGCCGTCTTCAGTTTTCACAAGTTTCACTCTCAACCCTAAACAGT
ACTTCTGTGAAGTACCCTTTGGCCCCTCGTTTTCAGCTCCTAAACTCACCTGGAAA
TAGATGTCAATCTAATTTTGGGTCTGACTAGTGCAGTAGGCATTTTTGGTGA

Sequence ID 782

CTCACACAGAACAAAAATGAATGAGTGTGGCTGTGTGCCACTATCACTGTGTCTAC
AAAAACAGCCAGTGGGCCTGATTTGGCCCTTGGCTGCAGTGCGCCCGTCTCTGTTT
TTGAGGAATAAAATCGCATCATTTCATATGGCTAATGCAATTTTTTTCCCATCTGG
AAGCAACATCTGATTGGACTCATCTTGTATGGTGCTTGTTACAGTCTCTGTAAATG
GGAGAGGGTCCGAGAATAGCTCTTCCTGTTTTCATCAGGACTGTTTTTAGGGATGG
CAAAGAAGTCAGTGTGTCCAGCCTGTGTCCTCCTCACCACGTGGCTGATTCCTGAA
TCTGCATGTGCANCACNTGCCGTTGTCTGGGGCATGATCTGTGTGA

Sequence ID - 785   nt: 556

CTTTTCTCTGGGTATAGATTTACCCTAGCACCTATCTCATTATATTGAATTTTCCA
GCATATTTAAATAAACTATTAATTAGTCACACTATTTCTTAAAAGTCACACTATCA
ACTAATCGTGACCGCAATTATCTAGGGGTGATAATCTGCTGAGTCTACTCTTTAAA
TACACTGGGACCCAGCATATTGAGTTATATTGGCACAGAAACTTCACTCTGGGTAT
AGATTTACCCTAGTACCTTGCCGGCAGGATCCTATTATTCATGGTTGTACAAGCAA
GGTTCAGGGAAGAGGCTGGCACAGAGAAGGTACCTGGTAACTGTTGTTTGAGGCTG
AATTCAGCTCAACTCAGCTCCAGTAGAGATGGTGTCCCCTTCTCTACCGTGTTGAG
ATAGTGTGCAGTCCCTTCCTAAGGGCTGTTACCCACCGCAATAGGACTTGTCAGCT
TCAACTTTTAAATTTCTCTGCTCCCGCTGGGACCCACCCGCTTCAAAAATCATCAT

GGNGGNTTTAGCACCAATTTAGTAAACACAAACTGTCTGAAATATTTTGGAT

Sequence ID 796
GAACATTCAAGATAGTGAGAGGAAGAAAAAGATATGGCTGTACGGGACCGAGGTCT
CTTCTATTATCGCCTCCTCTTAGTTGGCATTGATGAAGTTAAGCGGATTCTGTGTA
GCCCTAAATCTGACCCTACTCTTGGACTTTTGGAGGATCCGGCAGAAAGACCTGTG
AATAGCTGGGCCTCAGACTTCAACACACTGGTGCCAGTGTATGGCAAAGCCCACTG
GGCAACTATCTCTAAATGCCAGGGGGCAGAGCGTTGTGACCCAGAGCTTCCTAAAA
CTTCATCCTTTGCCGCATCAGGACCCTTGATTCCTGAAGAGAACAAGGAGAGGGTA
CAAGAACTCCCTGATTCTGGAGCCCTCATGCTAGTCCCCAATCGCCAGCTTACTGC
TGATTATTTTGAGAAACTTGGCTTAGCCTTAAAGTTGCTCATCAGCAAGTGTTGC
CTTGGCGGGGAGAATTCCATCCTGACACCCTCCAGATGGCTCTTCAAGTAGTGAAC
ATCCAGACCATCGCAATGAGTAGGGCTGGGTCTCGGCCATGGAAAGCATACCTCAG
TGCTCANGATGATACTGGCTGTCTGTTCTTAACAGAACTGCTATTGGAGCCTGGAA
ACTCAGAATGCAGATCTTTTGTGAACAAAATGAAGCAAGAACCGGAGACNCTGAAT
AGTTTTATTTCTGTATTAAAAACTGNGATTGGAACAATTGAAGA

Sequence ID 801
CCACTCCACCTTACTACCAGACAACCTTAGCCAAACCATTTACCCAAATAAAGTAT
AGGCGATAGAAATTGAAACCTGGCGCAATAGATATAGTACCGCAAGGGAAAGATGA
AAAATTATAACCAAGCATAATATAGCAAGGACTAACCCCTATACCTTCTGCATAAT
GAATTAACTAGAAATGAGGATTCTGACCTTGACTTTGATATCAGCAAATTGGAACA
GCAGAGCAAGGTGCAAAACACAGGACATGGAAAACCAAGAGAAAAGTCCATAATAG
ACGAGAAATTCTTCCAACTCTCTGAAATGGAGGCTTATTTAGAAAACAGAGAAAAA
GAAGAGGAACGAAAGATGATAATGATGATGAGTCAGGTAAAAGTTCCAGAAATGT
GAACAACAAAGATTTTTTTGATCCAGTTGAAAGTGATGAAGACATAGCAAGTGATC
ATGATGATGAGCTGGGTTCAAACAAGATGATGAAATTGCTGAAGAAGAAGCAGAAG
AAGGAAGCATTTCTGAAATATGAATGAAAAAAATTACATCTTTAGAAAAAGAGTTA
TTAGAAAAAAGCCTTGGCAGCCGTCNGGGGGAAGTGACGCACAGAAGAGACCAGAG
AATAGCTTCCTGGANGAGACCCTGCACTTTACCCATGCTGCTGGATGG

Sequence ID - 808   nt: 641
CCGGGTTTTAGTATTTAACCAAGAGCCTTTTAAATATTGAAAACCCATAGTTCAGA
AAATGTTAGTATTGCTGCCCTTCTTCACATAAATTTTTTTTTAAATTATACTATTA
TTTTGCTTAATTTTATATTGGGTTAAAACAACCTTCAAGAAGGTTAACTAGGAAAG
AAGACCTTTTTGTTTTATTTTTACTATTTATATATAGAAGACAAATCAGCATTTGG
TGATAGTTTTACATGACCAGTTATCAAACGGTCATAGTATGAAGTGTGCAGTTGTT

- 221 -

CATTATTAGTAAATTATGTTTGATTTTTAAACTATTTAGTACTAATAGTTGAGATG
AAAACTGAAGAAAAATGCCAATGTGACGTTTGTGTATAGCTAGCCTTAAAAAACTT
CCCATGTTTTTAGGTGACTTTTTTCCCCCTCTTAGTACTCTGGAGAAACAATGAAG
ATGGGCCATCTCAATTCCAGATGTAAACAAAAGTAATTTTTATTTCAACATTTAA
TGTAACTGCTATTATTGNGGATTCTTGNCTTGNGTATTTTCTTTCCCTTATTCAAG
TAATATAGAATAACTTTCCTTAAAATGATTTGATCCAAGATACGTCATTTCTGTAT
TGGCAAAATGCCNCTATTAAAGTGT

Sequence ID - 814   nt: 132

GTTAAAGTGATACATTTTTATACCAAATGTGTTTATTTTTTTGTGCAAGTAATCCT
TAAAATTGCAATTGTATTAGGTGTTAAAATAAAGTTTTTAAAAAATTAAAAAAAAA
AAAAAAAAAAAAAAAAAAA

Sequence ID 817

GACAACCTTAGCCAAACCATTTACCCAAATAAAGTATAGGCGATAGAAATTGAAAC
CTGGCGCAATAGATATAGTACCGTAAGGGAAAGATGAAAAATTATAACCAAGCATA
ATATAGCAAGGACTAACCCCTATACCTTCTGCATAATGAATTAACTAGAAATAACT
TTGCAAGGAGAGCCAAAGCTAAGACCCCCGAAACCAGACGAGCTACCTAAGAACAG
CTAAAAGAGCACACCCGTCTATGTAGCAAAATAGTGGGAAGATTTATAGGTAGAGG
CGACAAACCTACCGAGCCTGGTGATAGCTGGTTGTCCAAGATAGAATCTTAGTTCA
ACTTTAAATTTGCCCACAGAACCCTCTAAATCCCCTTGTAAATTTAACTGTTAGTC
CAAAGAGGAACAGCTCTTTGGACACTAGGAAAAAACCTTGTAGAGAGAGTAAAAAA
TTTAACACCCATAGTAGGCCTAAAAGCAGCCACCAATTAAGAAAGCGTTCAAGCTC
AACACCCACTACCTAAAAAAATCCCAAACATATAACTGAACTCCTCACACCCAATT
GGACCAATCTATCACCCTATAGAAGACTAATGTTAGTATAAGTAACATGAAAACAT
TCTTCTNCGCATAAGCCTGCGTCAGATTAAAACACTGAACTGACAATTAA

Sequence ID - 821   nt: 370

AAAGAGCTCCCAAATGCTATATCTATTCAGGGGCTCTCAAGAACAATGGAATATCA
TCCTGATTTANAAAATTTGGATGAAGATGGATATACTCAATTACACTTCGACTCTC
AAAGCAATACCAGGATAGCTGTTGTTTCANAGAAAGGATCGTGTGCTGCATCTCCT
CCTTGGCGCCTCATTGCTGTAATTTTGGGAATCCTATGCTTGGTAATACTGGTGAT
AGCTGTGGTCCTGGGTACCATGGCTGGTTTCAAAGCTGTGGAATTCAAAGGATAAA
TTAATGAAGAAAACAAGCGGAGCTGAAGAAGAAAGTACAATATGGTGCTGTCTTCC
TAATGAAATAAATTCACTAAATGGACATTAAAAA

Sequence ID 825

- 222 -

AGACTCGAGCAAGCTTATGCATGCATGCGGCCGCAATTCGAGCTCGGCCACTTGGC
CAATTCGCCCTATAGTGAGTCGTATTACAATTCACTGGCCGTCGTTTTACAACGTC
GTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCT
TTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTT
GCGCAGCCTGAATGGCGAATGGAAATTGTAAGCGTTAATATTTTGTTAAAATTCGC
GTTAAATTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAA
TCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGG
AACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGT
CTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTTGGGGT
CGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAAAGCT
TGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAAAAAGCCAAANGGAG
CCGGCGCTAGGGCCTGGCAAGTGTACGGGCACGCTGCGCGTAACCACCCACACCCC
GCCGNGCTTAATGCCCCNTTCAGGGCGCGTNCTGATGCCGNATTTTNTCTTACNCA
TNTGTGCNGGNTT

Sequence ID 833
TAAAATAATGGCAAAAAACAAACAAAAAACAAGTTCTCTAAACAGAAAGGAAATTA
CTAAAGAAGGAATCTTGAAATAACAGGAAAGAGGAAATACCACAGTAGGCAACATT
ATGGGTAAATAAAACAGACTTTCCTTCTTTAGTTTCCTAAAATATGTTTGATGATT
AATGCAAAAATTACAATATTTTCTTATGTAGCACTAAAGGTATGTAGAGAAAATAT
TTAAGATAATTGTACTGTAAGCGGGAGATGACAGTGACATAAAGGCAACGTTTTTA
TACTTCACTCAAACTTTATGTATTAATGTAATCCATAAAGCAACCAAAAAAGCTAT
ACTAAGTACATTCAAAAACACAATAGATAAACCAAACAAAATTCTAAAGGATGTAC
AAGTAACCCACTGGAAGCTGCAAAAAATGTAAACAGAAACTAAAAACAGAGAATAA
ATGAAAAATTAAAAACGAAATGGCAGACTTAGGCCCTAATATACAAATTATCACAT
TAAATATAAATGGTCTAAATACACCAACTGTAAGACAGAGATTAGCAAAGTCGATT
TAAAAACATGACTCAACTACGTGCTGTCTACAAGAAACTCACTTCAAATATACCAA
GATAGGAAGGTTGAAAGTAAAACGATGGAAAAGATGTATCATGTGAACATTAATC
AAAGGAAAGCAGGGGTGGCTATATTAACATCAGGTAAAATAAACTTT

Sequence ID - 837   nt: 603
TGAGGNTGGTCATGATGCANAAGCTACTCAAATGCAGTCGGCTTGTCCTGGCTCTT
GCCCTCATCCTGGTTCTGGAATCCTCAGTTCAAGGTTATCCTACGCGGAGAGCCAG
GTACCAATGGGTGCGCTGCAATCCAGACAGTAATTCTGCAAACTGCCTTGAAGAAA
AAGGACCAATGTTCGAACTACTTCCAGGTGAATCCAACAAGATCCCCCGTCTGAGG
ACTGACCTTTTTCCAAAGACGAGAATCCAGGACTTGAATCGTATCTTCCCACTTTC
TGAGGACTACTCTGGATCAGGCTTCGGCTCCGGCTCCGGCTCTGGATCAGGATCTG

- 223 -

GGAGTGGCTTCCTAACGGAAATGGAACAGGATTACCAACTAGTAGACGAAAGTGAT
GCTTTCCATGACAACCTTAGGTCTCTTGACAGGAATCTGCCCTCAGACAGCCAGGA
CTTGGGTCAACATGGATTAGAAGAGGATTTTATGTTATAAAAGAGGATTTTCCCAC
CTTGACACCAGGCAATGTAGTTAGCATATTTTATGTACCATGGNTATATGATTAAT
5   CTTGGGACAAAGAATTTTATAGAAATTTTTAAACATCTGAAAA

Sequence ID - 839   nt: 71
ATTTATCTAATATTTGGTTTAATAAAATGTGAATAATGAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAA
10

Sqeuence 849   nt: 622
TTTTTTTTTATTTTTTGAGAATGGAGTCTTGCTCTGCCGTCCAGGCTAGAGTTCAG
TGGTGCGATCTCAGCTCACTGCCACCTCACCTCCTAGGTTCCAGAGATTCTTGTGC
TTCAGCCTCCTCAGTAGTTGAGAATACAGGAACACGCCACCACGCCTAGCTAATTT
15   TTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTC
CTGGCCTAAGTGACCCACCTGCCTCAGCCTCCCAAAGTGCTGGGATTATAGGCGTG
AGTCATTGTCCCCAGCCGGATGTTTTCATCTTGATTTGCCTTAGTTTCTAAATCTC
ATCCTCTCCATTTTCTCCTGTTAGTAGTCACAGAGAACCAAATTCTGTCAAGTTAT
GAAACTAAAGTCTCTCTTCCACAAGTCTTCCTGTGTTCTGCCTCAAGTGAACTTGA
20   AAGAACATCAGTTTGTGGGAAGGTTGAAGACCGAATGATCTGCTGGGAAATCACTG
AGGCATTGCCATTCTCTTGAGGAATTTCATTTTCATCGAAGTTTCGGTTTATATCC
CTTTCTTGGTGAGTACTATTGCTGTTATGTAAATTAAATGAGTCGTCATCCTTCTT
NTGAGC

25   Sequence ID - 860   nt: 501
GTGAAATCACTTTCATGGATTATTAATGGATTTAAGAGGGCATCAATCAGCTCAAC
TCAAGATTTCATAATCATTTTTAGTATTTAGATTGTGCCTCAAAGTTGTAGTACCT
CACAATACCTCCACTGGTTTCCTGTTGTAAAAACCTTCAGTGAGTTTGACCATTGT
GCTCTTGGCTCTTGGGCTGGAGTACCGTGGTGAGGGAGTAAACACTAGAAGTCTTT
30   AGTACAAAACTGCTCTAGGGACACCTGGTGATTCCTACACAAGTGATGTTTATATT
TCTCATAAAGAGTCTTCCCTATCCCAAGGTCTTCATGATGCCAGTAGCCATATATG
ATAAATTATGTTCAGTGATAACTTAGTTATCAGAAATCAGCTCAGTGGTCTTCCCC
GCCATGATTCACATTTGATGAGTTTTTAAAAATCAAAGTGATTTTGAAAATCTCTA
ATGGCTCAGAAAATAAAAACATCCAGTTTGTGGATGACTATATTTAGATTTCT
35

Sequence ID 864
TTGTGTTTTTAGGACTCCTTATCTAAATTAAGGCAGAGAAGTTACAGTATTTATAT

CTGCATTAAATCTCAATTCCAGAAAAACCTTTTGAAAAATTATTTAATCCTCTGGA
AACTATTGATATGATACAGGAGAAATTTTCAGAAGTTTATTGAATAATTTAATATC
ATTTAATAGGACACTCTGGCTTGTATATAAGCAGATACGTTACTCAGACTTCTTGG
CTGTACTCTAAAATAATATATGTACTAGTCTCCTAAATATTACTAGCTCACCTTTC
5   AAAATGCATACTAATATTTCAATGTCTTTCTTCAATTTGAAAAGCTCTTGAATATC
TACTTGTGATAGCCCTAAGAGCTGAGATAATTATTTCCAGGAGGTTGAATCCCTGA
TTCTTAACTGTTCAGCAATGCATAAGCAAGAGAGAATATGACATAAGAGGACCATT
TCTACATTAGCCATTTTTTTTCACAAGATACCTATGTGAATACAGGGCACCTGGGA
GGGTAAGTGGAGGACTATTTCTAACTATATTTATAAGCACATACTGATATTGGTGA
10   ATCAAAACCTACAGCAGTGCTTCTCAGATGGGAAGGGAGACAATGTGTAAGGAGAT
CAGGAATTCATTAG

Sequence ID - 865
CCANAATCCACTCTCCAGTCTCCCTCCCCTGACTCCCTCTGCTGTCCTCCCCTCTC   nt: 122
15   ACGAGAATAAAGTGTCAAGCAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAA

Sequence ID 867
TTTTTTTTTTTTTTTTTTTTCAGAGTCACAGATATTGTATAGCTGAGGTAAGCATTT
20   TACAACTTTTCAGACACAAGTAAGTACATAAATATTATTTTACAACCAACAATNTT
TAATATTTCCACATTGAANAATAGATGTGATAATTAAATCTTTTATAAGGTTTTAA
AAAGACATGAAACATAAACCTAATTATACATAAAAGAAAGAATTTTAAACAAGAG
CTTATTGNGATGACATTACTCATAACTTTTACCTTTAAAACCTTTTCTTGGGTAGC
TATTCAAAAGTAAAGACCACAAGTTTTGTTGCCCANATTTCTTATGTTTNGTATAT
25   TTAAGCTCTTTATTTATTGAACAGATGNGTCATTAATTCATTNGGAGCATTACTAT
TATCAGTAAAATTTGATTTTTTTTTCCCCTCAGTCATAGGTAAATCAGCTCCACCT
GGAATTTCTAAGGACCCAGTTTTAGTCAATATTTTCAAGTAATCATGACCTCAGAA
ATAGTCTTAATTAAGATAACAAATATTAGCCATCAAAATGGAACCAAGACAAGATT
CTAATGTTTGTAAACAGTCAATCCATATTTATGAATATTAGCATATATTGGNGAAT
30   AGTTAAGGCAAAAGGGTCTAGCAG

Sequence ID - 869
TTGTGTTTTTAGGACTCCTTATCTAAATTAAGGCAGAGAAGTTACAGTATTTATAT   nt: 667
CTGCATTAAATCTCAATTCCAGAAAAACCTTTTGAAAAATTATTTAATCCTCTGGA
35   AACTATTGATATGATACAGGAGAAATTTTCAGAAGTTTATTGAATAATTTAATATC
ATTTAATAGGACACTCTGGCTTGTATATAAGCAGATACGTTACTCAGACTTCTTGG
CTGTACTCTAAAATAATATATGTACTAGTCTCCTAAATATTACTAGCTCACCTTTC

- 225 -

AAAATGCATACTAATATTTCAATGTCTTTCTTCAATTTGAAAAGCTCTTGAATATC
TACTTGTGATAGCCCTAAGAGCTGAGATAATTATTTCCAGGAGGTTGAATCCCTGA
TTCTTAACTGTTCAGCAATGCATAAGCAAGAGAGAATATGACATAAGAGGACCATT
TCTACATTAGCCATTTTTTTTCACAAGATACCTATGTGAATACAGGGCACCTGGGA
NGGTAAGTGGAGGACTATTTCTAACTATATTTATAAGCACATACTGATATTGNTGA
ATCAAAACCTACAGCAGTGCTTCTCAGATGGGAAGGGAGACAATGTGTAAGGAGAT
CAGGAATTCATTAGTCACCTTTCAGATGGTTTAATGCATACAGCTGTACCG

Sequence ID 870

GGAGTTTGAGCAGATCCTTCAGGAGCGGAATGAACTCAAAGCCAAAGTGTTCCTGC
TCAAGGAGGAACTGGCCTACTTCCAGCGGGAGCTGCTCACAGACCACCGGGTCCCC
GGCCTTCTGCTCGAGGCCATGAAGGTGGCTGTCCGGAAGCAGCGGAAGAAGATCAA
GGCCAAGATGTTAGGGACACCAGAGGAAGCAGAGAGCAGTGAGGATGAGGCTGGCC
CATGGATCCTGCTCTCCGATGACAAGGGAGACCATCCCCCACCCCCGGAGTCCAAA
ATACAGAGTTTCTTTGGCCTATGGTATCGGGGTAAAGCTGAATCCTCTGAGGATGA
GACCAGCAGCCCTGCACCCAGCAAGCTAGGGGGAGAAGAGGAGGCCCAACCACAGT
CTCCAGCTCCTGATCCGCCCTGTTCTGCCCTCCACGAACACCTTTGTCTGGGGGCC
TCAGCCGCCCCAGAGGCCTGACTTAGGGGTCTGGCTGTGGAAGGATGTGTGGCCTC
AAATGAGGACAGGGCTCCCGCCTTCACAGCCCTCGCCAGGGGTCTGCCCCAATCCT
GGCCTGCATCAGGCAAGGACGGGGTCTCAGC

Sequence ID - 871   nt: 642

GCAAGTCTTCAGTATGTACATTTATCCCCTAGAAGAAGAAAAATTAGTTGTGCATG
AAAAAGAAACATTAACTGCAAAGCTAAATGCTCACACTCTAAATCAGTGCTCTCCA
AAGTACAGCAGGCGGGAAAAGAAAATGGTAGATTTTTTTCTTCCAATTACTTTAAC
TTATTCTTTTTAATGGACACTTCATACATAAATATATTCACAATATATTAATATAT
ACATAATGTATAAGCATACATATTGAATGTGCAGTCAAAAAATGTACTAATGGAAT
GCTCTACCAAAACAAGTTCACGTTCATCTGTAAAATGGGAATAATATTTTTAAAAG
GCATACAGTCTGAACATTTTTAGATTATTCATAAAATCTATTCAGAAAGTTAAACT
AAAAAATTTAACGTATGCCTATAACAAATTTTGTACTTAATGTAATTGNTTTTCAT
CCTGAGATCTAATATCCTCGTTTTTAAGTAGAGCCACTTGTTTGCTACAGTTTAGT
CAAAACGTTAACATTAGATGGGTAAAGTAATATGAAATCTTTCTACTACTCCAAAA
TAGAAAACAGAACATTAAAAAGATAAAAATTCAAACATACTTACCAGTAGATTTTC
AACTGNGCAAAAGCTCATTGCATGGG

Sequence ID 873

GTTTTCCACCGTGAAGAGAACATTTCCTCTGGGAATGACAAAGCCCTCAGGAACNG

CTTTTATTTCTATTGGAAGATGCCCATCATACTTCTGGCAGGATAAAATGATAAAT
TTATTTATTCAACAGATGATACTCAATTCCCTGCTGTTTTACTAAAGGTTCTTTAC
GTTTTATAGAAGCTAAATTTACTGTCATAGAAATTGCAATTGTAGATGTTACTGTA
ATCTAGTCAGAATATCCTTATCCTTCTAAAATAAAACTAGTTAAAATTATTAACAT
ACGTACTGATATTAATTTTTAAGTTTAATGCTGCCACGTGCTTCTGCTAAGAACAT
TTATCACTACAAGTGGCAGAAAATTCCAAACTCATCAAAACCAAACTGTTGCTTCT
TCCCTGCTTTTTCAGAAAATGAGAAGGATGACTTTATTCCAACATATTCTAAAAG
TATTCCAAGAACACTACCTTTATTCTAAATTCGTTATTTTCACAAAATAAAGGCTG
CAGATTGAAAGATAAAGGATTGCTATTAAAGAACAAAAGAAAACAAAACCGAGAGA
GAAGGAGAGCTAGGAAATCCCTGCANAANAACCGAATANGGTCCCTCTATTCTGG
GCCGGGGCCTGAAACTATGAAACAGGCCAACACAGAATCTTGGCA

Sequence ID 875

CCTCTGACTCGCTCAGCTCACCCACGCTGCTGGCCCTGTGAGGGGGCAGGGAAGGG
GAGGCAGCCGGCACCCACAAGTGCCACTGCCCGAGCTGGTGCATTACAGAGAGGAG
AAACACATCTTCCCTAGAGGGTTCCTGTANACCTAGGGAGGACCTTATCTGTGCGT
GAAACACACCAGGCTGTGGGCCTCAAGGACTTGAAAGCATCCATGTGTGGACTCAA
GTCCTTACCTCTTCCGGAGATGTAGCAAAACGCATGGAGTGTGTATTGTTCCCAGT
GACACTTCANAGAGCTGGTAGTTAGTAGCATGTTGAGCCAGGCCTGGGTCTGTGTC
TCTTTTCTCTTTCTCCTTAGTCTTCTCATAGCATTAACTAATCTATTGGGTTCATT
ATTGGAATTAACCTGGTGCTGGATATTTTCAAATTGTATCTAGTGCAGCTGATTTT
AACAATAACTACTGTGTTCCTGGCAATAGTGTGTTCTGATTAGAAATGACCAATAT
TATACTAAGAAAGATACGACTTTATTTTCTGGTAGATAGAAATAAATAGCTATAT
CCATGTACTGNAGTTTTTCTTCAACATCAATGGTCATTGNAATGTTACTGATCATG
CATTGGTGAGGNGGTCTGAATGTTCTGACATTAACAATTTTCCAT

Sequence ID - 876   nt: 115

AAACTTTTGTGGCAACAGTGCACTAATTTGGATAATGTTTGTTCCCAATAAATTAA
GAGCCAAATTGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

Sequence ID - 878   nt: 634

GCCAGGCTTTGTGAATTACAGGACATTTGAGACAATCGTGAAACAGCAAATCAAGG
CACTGGAAGAGCCGGCTGTGGATATGCTACACACCGTGACGGATATGGTCCGGCTT
GCTTTCACAGATGTTTCGATAAAAAATTTTGAAGAGTTTTTTAACCTCCACAGAAC
CGCCAAGTCCAAAATTGAAGACATTAGAGCAGAACAAGAGAGAGAAGGTGAGAAGC
TGATCCGCCTCCACTTCCAGATGGAACAGATTGTCTACTGCCAGGACCAGGTATAC

- 227 -

AGGGGTGCATTGCAGAAGGTCAGAGAGAAGGAGCTGGAAGAAGAAAAGAAGAAGAA
ATCCTGGGATTTTGGGGCTTTCCAATCCAGCTCGGCAACAGACTCTTCCATGGAGG
AGATCTTTCAGCACCTGATGGCCTATCACCAGGAGGCCAGCAAGCGCATCTCCAGC
CACATCCCTTTGATCATCCAGTTCTTCATGCTCCAGACGTACGGCCAGCAGCTTCA
AAAGGCCATGCTGCAGCTCCTGCAGGGACAAGGACACCTACAGCTGGCTCCTGAAG
GAGCGGAGCGACACCAGCGACAAGCGGAAGTTNCTGAAGGAGCGGCTTGCACGGCT
GACGCAGGCTCGGCGCCG

Sequence ID 879

GTTGCCGGGTCCTGTGATAACTCTGTTTAACATTTTGAGGAACTGTTGAATGGTTT
TTCACAGCAGCTGCCTCATTTTTTATTCCCATCAGCAGTACTTCTTGGTTCTAATA
CCTCCACGTTCTCGCCAACACTTGTTGTTGTCTGTAATTTCGTTGTTAGCCATCCC
AGTGGGGATGAAGTAGTATCTTACTGTGGTTTTCAGTTGCGTTTCCCTGATAATTA
ATGATGGTGAACATCTTTTCATGTTCTTGTTGGCCATTTGTATGTCTTCTTGGGAA
AAAAAAATGTCTGTTCAAATCCTTTACAAAGTATTTATTTTTTATGTCAACAATA
TAACCACTCAGTACACTGCTTTTTANACAATGATCTTTTAAAGGTTTGTTTACAAC
ATTTAGCACTTGAAATTTTAAGGTTATGCCCTCAAAAAAATTGCTGAGGGAGCTAA
GCTATGAAGATGCAAAGGCATAANAATTATACAATGGACTTTGGGGGAATCCAGGG
AAAGGGTGGGAGGGGGGTGANGGA

Sequence ID 881

TCGACTCTGATTTTTTTTTCTCCTTCCTCGCAGCCGCGCCAGGGAGCTCGCGGNGC
GCGGCCCCTGTCCTCCGGCCCGAGATGAATCCTGCGGCAGAAGCCGAGTTCAACAT
CCTCCTGGCCACCGACTCCTACAAGGTTACTCACTATAAACAATATCCACCCAACA
CAAGCAAAGTTTATTCCTACTTTGAATGCCGTGAAAAGAAGACAGAAAACTCCAAA
TTAAGGAAGGTGAAATATGAGGAAACAGTATTTTATGGGTTGCAGTACATTCTTAA
TAAGTACTTAAAAGGTAAAGTAGTAACCAAAGAGAAAATCCAGGAAGCCAAAGATG
TCTACAAAGAACATTTCCAAGATGATGTCTTTAATGAAAAGGGATGGAACTACATT
CTTGAGAAGTATGATGGGCATCTTCCAATANAAATAAAAGCTGTTCCTGAGGGCTT
TGTCATTCCCAGAGGAAATGTTCTCTTCACGGTGGAAAACACAGATCCAGAGTGTT
ACTGGCTTACAAATTGGATTGAGACTATTCTTGTTCAGTCCTGGTATCCAATCACA
GTGGCCACAAATT

Sequence ID 883

TCATTTACATTAATACTCAAAACTGCTCGATTAAGCAGGTGCTGTTCTTATCGCCA
TTTTGCATATGATGAGAAAGGGTAAGGTCACCCAGCTAGTATTTGGCTCACAGCAG
GCCTTAAGACTTGGTTTGTGTGACTCATCAGTCCACGCTCCTAAAACCACTAAGTT

- 228 -

GTTCTACCCTTTAATGTTGAATTAACATTGGATAGTGTTCAAGTTTANATGGGTGG
GTGAGGGCCCAAGGACCTTTCAAACTCAGATCTCTTATTTAATAACCTGGTCCCAG
ATCCATTCCTCTGTCGAAGAGGAAGTCATCCTTCAGTGGCTATTCATTGTGGGGTT
AAGAGCGCAGACTATGAATTCAGTCTTTTTGGGTCCCAGTTTGCCAGACCTTGAGT
GAGTGCCCCGAGTTTACTTACTTGTAAAGGTAGGTGGAGGTAATATAATTAAATAA
ACTTAAAAACTAATTAAAAACAAACAAATGAACTAAGGTCTTAGGATATCTGGC
GTCTATTTTGCGCCAAATCACATAATGTCTATTGTTGTGTGTTGGACTATAGGATT
GTCCTTTAACAGGGAAGGGTTTATTTCTGTAATCAAGTCTGTCAATATTATGACCA
TGTTGATAATAGCTACCTTTAATTGAGGGCTTCCATGTGCCAA

Sequence ID 885

TCAGTGGAAAAGGGCAGGTTGAATCAAGGTGAATCAATCTGAAATTGAGCACACCT
GCCTGCCATCGCTGTTCCTTCAACTGAGTGCTGCACATCATGGGCTCTGTCTGTGA
GAGAAAAATCCCGGTGCTTGGTGTCCTTGCATGACATGGAGTTTTGCATGTAGATC
AATTTAAAATGTACCTCTTGTTTACATAATTTGCATAATTTTAAAAGATAATGTTG
CCAAACTTTGGAAATGTTAATGTTCANACTGAAAATCTCCACTACATGTAACTTTC
TTCCTCTGGATCAGTGGCATGGCTTATAATCCCAGCCAGTGGTTTGAACTGTTCCA
GTGTCAACTGCCATGTGCTCTGCTTCAAGGGGGAACTAGCCTTTTGTGAATTTTTT
GTACATAAGTATTTGTTACAAATATTTAGCAAATGCTTTCTATTTCTCTTGCTTG
TGCATATCTTGGCTGGCGTTACAGAAAAATAGTGTAAACATTATTTCCTTACCGGG
GAATGAGGGTTTT

Sequence ID 887

AGCACCTGGCACAGAGTAGTAGCTAACACAGATGTTAATTTTGCTGCGTCAAATGT
TTTCACTTTGAATCTCTCTTGAGTATTGTTCTCCTTATTGATTACATGATGACATC
CTGTTTTCTCTCCCTGACCTTTACTGTTTGTTTAGAAAAAAAAAAAAAAAAAAAAA
AAAAAA

Sequence ID 889

CAGAGAGCTTGTTCCCTCCCTCCCTGTGCATGCAAACAAGAGGGCATGGGAGCACA
CAGAGAGATGGCAGCCACCTACAAGCCAAGAGGAGAAGCCTCACAATCAAACTCTC
GCTGCTGGCGAGAGTCTTGGACTCTGTCTTGGACTTCCAGCCTCCAGACTGTGAGA
AACAAATTTCTGTTGTTTCAGCTTCTCAGTCTCTGGTGTTTTGTTATTGCAGCCTG
AGAACACAGCTGTACNATTATNAGGGAAACAGAAACACTGATACTTAACAATGCT
AATGCAATTATTTATTTGCTTTTCAGTCTCTACAAAACGTTCTAAAACACTAATCT
AAATATTAACAGTAAAATATTTGCATAACTAATGGAAACTAAGAAATCATATGACC
AATATTTCACTTATTGGTAATCTTACTCTACTGATTTCCCCCCAGACTGTGATTTT

TGAACTTCCTTGCCTTTCTCCTGTCTTTCTGNGTTTATTCATGGAATTCCAGTTAT
CTGGGCTTGAAATTGCAGGCTCTCCTAACTTAAGCAAAATCTGACAGATCAGCAAA
ATGAGATAAATGTTTCTTTTTTCTTTCTGACTGCATTAAATCAGATACAACTCAGC
ATTAAAAAGCTATCTTTGNAAAATGNTGGTACTAATAAATTAGTCTTA

Sequence ID 890

CCAGTTCCACATTCAGTGAAGTCATGAACTTGAAATTGGCCATGATCAAAAAGTAT
TTAAATCACAGAAGTTGCAAATGCCACAAATCAAGGTCTTTTTCTCTTGGAGAACC
TGTTAAACATTTACCAACTCACGACCGCCATGCACCCAATACTGCAATAGGTCTAT
AGATGCAGATACTGTCTCCATGAATCTTATAGGCTAGAAAGGAAATAGATAAGTAG
TCCTACCAGAAGAACATGATGAAGGCATTTGTGGTAAACAGAATGATGGCCCCCCA
AAGATGTCCACATCCTAATCCCTGAAGCCTATGAATATACTACTTTACTTGGCAAA
AGGGACTTTGCCACAGGTTTTTAATTAAGGACCTTGAAATAGAGAGATTATCCTGG
ATAATCCAGATGGCCCCAGTGTAATCCCAAGGGTCCTCACAAAGGGTAGGAAGGAG
AGCCAGAGTCAGAGAAGGAGACGTAGCAATGGAGGCAGAGGTCANAGAGAGATCTG
CAGATGCTGCTGTGTTGGCTTTGAAAATGAGGAATGCAGGTGACCTCAANGNGCTA
GATGATGCAAGGAAACAAATAATCTCCTATGAACCCTAGGATGGGCATTATTATGA
GTCCTATTTTATAAACAAGGAACTGACNTCCAGAAAGATAAATGC

Sequence ID - 891   nt: 626

GGCAGAGGTTGCAGTGAACTGAGATCATGCCATTGCAATCCAGCCTGGGCAACANG
AGTGAGACTCCATCTCAAAAAAAAAAAAAAAAAAGACAAGAGTNTCCACTCTAAACA
CTTNTATTCAACATAGTCCTGAAAGTCGTAGCCACAGCAATTTAACAAGATAAAGC
AATAAAATGTATTCAAATAGAAAAAGAGGAAGTCAAATTATCTTCACTGGNGATAT
AATTCTCTACCTGGGAAACTTCACCGAAAAGATTTCACCAAAAGATTTCTAAGCC
TAAATAATGACTTCAGCAAAGTCTCACCATACAAAATCAACATACACAAATGAGTA
GCATTTCTGTGCACCAATAATATTCAAGCTGAGAAAAAAGAACATGGTTCTATTT
ACAATAGCTACAAACAAAAAAATATGTACCTAGTAATACATTAAATCAAGGNGGTA
AAATATCTNTACAACAAGAACTACAAAACTGCTGAAAAAAAATAGAGACACGCAAA
TAAGTAAAAAGGCACTCCATGCTCATGAATTTAAAGAATCAATATAATTAAAATGT
CCGNGCTGCCTAAAGCAACTTACAGATTAAAGGCTATTTCTCTCAAACTATAAATG
CACCTTTTTA

Sequence ID - 893   nt: 585

GTCATTGCTGGGTGGCGCCAGCCCTCAGACTTGCCTCTTTGCAGTAGGAAGAAGGC
CTCCCCACATACCTTCCCACACTCATCACCTTAAGCCAGACTCGGTGTCCAGTGAA
TATGACCATCTCTTGCCCATTTTCTAATGAGTGTTTTCATTAATGAGTTATAAGAA

- 230 -

TGTGGTGGGTAAATCTATGGGCTTTGAACTAGTGAATCAACTTGGTTTCAGAATCT
GGCACTGCTACTTACTAGTGAATTTAAGCAAGTTATTTCACCTTTCAGAGTGTCAG
TTCCCTCATGCATACAAGGAAGATAAAAAATAATGTNTACNAAAGTATTGGAGTAA
TTAATACATGGAGAACTACATGTAAAGCGTTTAGCATGATGTCTGACATATTAAGC
ATCCAATATTAGTNGCTTGCAGAATTATTAGTAAAAGAGATTGCTTCTGAAAGCCA
TTCCAATTCTTAAATTTTATAATGCCACATTTGAGGTCACCTGAAGTCGTGTATAA
CATGTGTACATTTTTGCGATTTATTTTTTCAATTCCCANATTAAAGGCATAGAGAT
ATCCTAGCNANGGACTCCAAGTGTG

Sequence ID - 895   nt: 560
GTAATTGCAGCCTGGGCAACGGAGTGAGAGACTGTCTCAGGAAAAAAAAAAGAAAA
AAAACTACTGAGGTAGTTGAATATATCCTCCATTCCCCATTTGTGGATTAGTTAGT
AAATGGGGCATCTTAGGGTTTAAATATGTCCAGGGTCACTGAGGATCAGATCCTAG
GGTTCCTTTGACTCAAGGCTTTTGTCTCAGCAAAACGTCACCTTCCAGCAGGAAGG
CTTTCTCAGGCAAGTAGCAGGGTGGCTACTATGTATCGCTTCTTTATTTTTTCTTT
TTTAAAATAATGCAGGCACCGTGCGCATAATTTAAAAAATCAGTGCTAAAACCCTT
AAAAAAAAAAAGCTGTTCTCATCTCCTGTCTTTCTTTTTTTTTTCTTTTTATTTTT
TTCTTTTATTATTATTATACTTTAAGTTTTAGGGTACATGTGCACAACGTGCAGGT
TTGTTACATATGTATACATGTGCCATGTNGGTGAGCTGCACCCATTAACTCGTCAT
TTAGCATTAGGTATATCTCCTAATGCTATCCCTCCCCCCTCCCCCCTTTTTTTTTT

Sequence ID 896
GGGAATGTCTTAGGCACTGGGACTGTAAGTGCAAAGACCCTGTGGCACAAGGGAAT
GTTAATTATCTACCTTTCANAAACTGGAANAAGGCCTAGCCTAGAGCATTGAAAAC
AATAAGGGAAAGGAGGAGTAAGGCTGGANAGATAGGAATGGTTTAAAGTCTTTGTT
AAAAATTTTTTTAAAAAAATCTTTATCACAAGAAGAGGATTGGCNTGATCAAATTT
GACTTTTAAAAANATTACTTGGGTTGGGCATGATCAAATACTACTTAGGGAGATTA
GTTTANATGATAATGGCATTCTGGACCANAGTGGAGTCAGAGGTGAAAAGAGGTAG
ATATTCCANAATTGAGGGATTTGTGAGGTGAAATCATTTGTTACAGATATTAAAGG
ATAAGGAGCTTTGTCAAAGGGGATCTTAAGTTTCTGGTATGGTAACTGGGTTAGAG
AGCCCTGGAACATGACCAGCTTTAAGGGAAGAGAGCTTGAGCTCTGTTCTTGTTAA
GCTCAGTTTGAGATCTTTGTGGAATCAAGTGGAGAGGTCTAAGCAGGGAACTGGCT
TGGCTAGGCTGTAAAGATGAATCTGAGAGTCCCAAGAATATGGTAATTATTAATAA
AAGCCTTAGGTANATGAAATTGTTTTGGG

Sequence ID - 897   nt: 509
GCAAATCTACACATTTGATTAAATGATAGGGAACTATGCACACACATAATACATAT

AATGCTAGTTTCTTGGTTTTGATATTGTACCATAGTTATGTAAGATGTAACCATTG
GGGGAAACTGGGTGAAGGCTACATGAGACCTCTCTGTACTTAATCTTTGCAACTTA
TGTGAATCTATAATTATTCCAAAATAAAAAGTTTTAAAGAACCTAAGTATCCTTAT
TACTGAGGGTCATCGTGCTAGACAGCAAGGTTGGGCCAGAGCTTCTAGTTATTTAA
AATACTAAATACCAGCCTGGGCAACATAGCAAGACCCTGCCTCTACAAAAAGCAAA
AAAATTAGCTGGGCATGGTGGTACATGCCTGTGGTCCTAGTTACTCTTGGAGGAGT
CTGAGGTGGGGAGCTTGAGCCTAGGAGTTTGAGGCCGCAGTGAGCCTTGATTGTGT
CTCTGTACTCCAGTCTGGGCCACAGAGCAAGACCCGGTCTCTAAAAATAAATAAAT
AAATA

Sequence ID 898

ANTGCACTCCAGCTTGGTGACAGAGGGAGACTCCATNTTAAAAAAAAAAAAAAAAA
AAAAAAGGGAGTAGCTTGAAGCCACATAGTAGTTAGTGGTAAAGGCCACCCCTTT
TCCCACAACTCACACCAGCACCACAAGCTAGCCTTTNTAATTTCCAAGCCAGTGCC
CTTTCAACGCACACACCCCTGTGTCAGTTCCCTTTCTGCTGCAAGCTCTCTGGAGG
CAGATACTGTTGAGTCCCTGGCCTGCCTATGAGAACGGCTCATGATCTCTATTTCT
TCTGCTTAATGACCATCTCGAAGTAACAAGTTTAGCCTAAAATAAACTTGCTAAGT
TAGCAAAGGAAGTCCTTAGCAGCCACCATTTCTCGATTCCTCCATCACCTCCCCTG
CCCCTCAACTCCCTCATTTCTCCCAAGATATGGGCTCCAGGCTGGGCGCGGTGGCT
CACGCCTATAATCCTAGCACTTTGGGAGGCTGAGGTGAGCAGATCACTGAGGTCAG
GAGTTCG

Sequence ID 899
TCNTTCGGAACGCGCC

Sequence ID 900
CTGGAGGGATGGGTAGGATTTTGACAAGAGTGGTTGAAGGTATTCTAATTCACTTA
GTACCTACATGTGCGAGGCAGCATGAAGGCAAAAAAGCCTGGGGCATGTTCAGAGA
ATAGCAAGTATTCTAGTTTGAGTGGCACCTGGTACGTATATAAGGGAATAGTAAAA
GATCTGGCTGGAAAGGAAAAGTAGGGGCAGGTTACGAAGGACCTCTGAAAGTCAGA
CTGTGGAACTGGAACTTTTATCAGGAAGCAGTAGTTAGTTTTTTCAAGCAAAAGCT
AATTAGAGTTGATATTTAGGAGGATGAATCTAACAGTTGTGTGCAAGGATGCCTTC
AAACTGAGTGAGACTAGTACTGGAGACTGGTTAAGAGACTACAACAATAACCTGAG
TAAGAATTAATACAGGCCTGACCTAGTTTTGAGTGAGTAGGATTGGAAACAAGAGT
TTTAGGTATTATAGGATTTATGCATATAAAATGGACTTGACAGAACTTGAAGAAAG
AGAAAGTGTCAAAAGGACACAGAAAGTGAGGCAGGATATCTTACAATGTTAAAGGA
AAGGAATAATAGAAGTTAC

- 232 -

Sequence ID 903

GGAAACATAAGCTTGTTTCAGTACACTCACGCTGTAGATTAATTCTGATATTACAT
ATCTCCATCAGACTTTGTACCCTCTCTCTTCCATCCCTTACCCTTACCGATTAGGT
TGGTATTACCTAAAAATCCATAGAAATGTCCAGGTGAATTGCCTTATGCTTTCTA
CCCCATAAGGTATAATT

Sequence ID 904

CTCTGTGGTGTGAGAACACAGTGGGTGACCAAGGCTTTCCAGATGAACCCAAGGAA
AGTGAAAAAGCTGATGCTAATAACCAGACAACAGAACCTCAGCTTAAGAAAGGCAG
CCAAGTGGAGGCACTCTTCAGTTATGAGGCTACCCAACCAGAGGACCTGGAGTTTC
AGGAAGGGGATATAATCCTGGTGTTATCAAAGGTGAATGAAGAATGGCTGGAAGGG
GAGTGCAAAGGGAAGGTGGGCATTTTCCCCAAAGTTTTTGTTGAAGACTGCGCAAC
TACAGATTTGGAAAGCACTCGGAGAGAAGTCTAGGATGTTTCACAAACTACAAAGC
TGAAGAAAATGAAGCCCTATTACTTGTTTGTAAGATTTAGCACCCTTCTGCTGTAT
ACTGTACTGAGACATTACAGTTTGGAAGTGTTAACTATTTATTCCCTGTTAAAATT
TAACCTACTAGACAATGATGTGAGTACCCAGGATGATTTCCTGGGGCACAGTGGGT
GAGGAGATGGGGACAGGTGAATGGAGGAGTTAGGGGAGAGGAAAAGTGGATGGAAG
TGTCTGGAAAGGGCACCAAAAAAGTCTTCCAGGTCTGATCCTGTTTCTTGCTCTGA
GTGCTAGCTACCACTGTGTCACACTGTAACATN

Sequence ID - 905   nt: 655

CTCAGCTCTTGCCTGGTCACCTTGTGGCTTTTACCATCCTCATCCCCTGTGCCACC
CACATCCTGCCACTTCTGCATGGAGTTGGGGTGGGGCCATTGGAGAAAAGAGGTTA
AACAAGCAGTAATTTACTTGAGTACAGTCTTTGAGCCAATGAAATGCCAGTCATCA
TTTCCAGGGGTACTTGTCATCTTGTCAACAACCCGCTGATAATGCTCCTTCAATG
TGAATAGCAAAAGTAGGGAGAGACGCTGAATGAAGAAGATGCCTACCCCTCAGGAA
GACTGCTGTCCGCCTCCAGGCCTGCATGCACACACCCATGCCCACCTGCACCCCCA
GCACCACGCCCACACTCACTCGCACACACCCACATGCCAGTGTTTTGGGGTTGGCA
GCCTGGACACTGCTGAGGCAAACACAAGTCATCAAGCATAATTCTCATTCTCTCCT
TCTGTCTCTGTTTTAGTTACAGGAATTTGGTCAGTTTAGAGGATTTAATAAGTCCG
TGGAAAATTTGTTTCTGTCTCTTGCTACCCACGTGAAAAGTAAGTGCATGCTTCAT
GATGTGTTTTCCCACTACCTTCCAGGCCAGCCGAGCCCACTGGCCANGGCCTGGCC
CGGTGACCTCGGTTGACACTGTCCTCANGCCACTCACTT

Sequence ID 906

CAGAATTTCATGTTTATGCTGCACAAGGCCTGTATTTTATAATGGTGGCTCTTTTG
GACGATGACTTCCTCGATGGTGAAACTTCCAGTAATCTCCCTCATCATACTGAAAT

- 233 -

GATATCAGTATATCATCAGAACACCATGGAGCTTGTCATTTGAGGGACACAGCTTG
CTTGTGTGCTTGGGAAAGAAGAGGTTTAGCATGGTTTCAGGTCAGTGATGAGTCCA
ATGATCTCTGCAAGTTCCCTTAGCTCTGANAATTCTGATGTCATATGCACTTCTGC
CGCCAGAGTTGCTGCTTACTGGATGCGTAAGAAGAAAAGAAAAAAAAAAAAAAA

Sequence ID - 907   nt: 582
CTTCCATTGGGGGTAAAGATCAAACTTTAGGCGAGCCAGGTCTGTATCTCCATTCC
TGTCTCTGACTGCTTCCCTGTAGGGATTGTCTGCAAGCGCACACCTGCATTTTCTT
GTCCACAAGTCTATGCTCTAACTCTGTCACCTGCATGGCTGCAAATTAGCTTCCTT
CTTCCTGCCCTCTTCTCTCTAGCTTGGATTTTGAATTTGAATGGCAGGCATGGGAT
GTCCGTGTGTGTGTACTGCTGATGTGTACAGCCGCTTGTTAGCGCTCTCATTGTCT
TCAAATGTAAGTCATTTTGGCTGGGTGCGGTGGCTCATGCGTATAATCCCACGCTT
TGGGAGGCTGAGGTGAGCTGATCATTTGAGGTTAGGAGTTCGAGACCAGCCTGGCC
AACATGGCAAAACTCCATCTCTACCAAAAATACAAAAATTAGCTGGGTATGGTAGT
GCACGCCTGTAATCCCAGCTACTTGGAATGCTGAAGCAGGAGAATTGCCTGAACCC
ANGAGGCGGAGGTTGCGGTGAGCCAAGATCACGCCACTGCACTCCAACCTGGGTGA
CAGAGCAAGGCTGTGTCTCAAA

Sequence ID 908
ACCTGACTTCAAACTATACTACGAGGCTACAGTAATCAAAACAGCATGGTACTAGT
ACAAAAACAGACCAATGGAACAGAATAGAGATCTCAGAAATAAAACTGCACATCTA
CAACCATCTGATCTTCAACAAACCTGACAAAACGAGCAATGGGGAAAGGATTCCCT
ATTTAATAAATGGTGCTGGGAGAACTGGCT-AGCCATGTGCAGAAAATTGAAACTG
GACCCCTTCCTTACACCTTATACAAAAATTAACTCAAGATGGATTAAAGACTTAAA
TGTAGAACCCAAAACGATAAAAACCCTAGAAGAAAATCTAGGCAATATCATTAAGG
ACATAGACATGGGCAAAAATTTCATGATGAAAACATCAAAAGCAATGGCAACAAAA
GCAGAAACTGACAAATGGGCTTCTGCACAGCAAAAGAAACTATCGTCAGAGTGAAC
AGACAACCTACAGAATGGGAGACAGTTTTTGCAATCTATCCATCTGACAAAAGTCT
AATATCCAGAATCTACAAGGAATTTAA

Sequence ID 910
CAAAAAACAAGAATTACCCGGGCTTGGTGGTGCATGTCTGTAGTCCTATCTACTCA
GGAGGCTGAGGCTGAAGGATCACTTGAGCCCAGGAGTTTGAGGCTGCAGTGAGTGA
GCCATGATCATGCCAGTGTACTCCAGCCTTGGCAGACTGAGCAAAACTTGGTCCCT
CGCAAAATGTTGAAGCCCAGTTTTCACTATTAACCTGTATTTCAGTTTCCCCATGC
TAACTTTGAAACACTGGGGCTGGCCTGAGGGTATAAAGGCTTATTCAAACTCAGTA
ATTTAAACTTAAAATCCTAAGGAACTTCAAAAAGTGTAATCTAGTCCAAATGGGGC

- 234 -

ATCAATTCTAAAGCATTTGCTTGTTTGAGCAGATTTTCTGTGTCTGAGGTATATAG
ATAACTTATCTTTTTATGACTAAATCCAAGTCCTTAGTTCCTGTTGGAATTCAAAA
TCATATTTAAAAATTGATGCTTTGTTCTATAATTAATGCTTTGATTGTATAAATAA
TAAGTATTCTTCCAAATCCCTTTTTACAGATGATGATTCTGATACCGAGACGTCAA
ATGACTTGCCAAAATTTGCAGATGGAATCAAGGCCNGAAACAGAAATCAGAACTAC
CTGGNTCCCAGTCCTGTNCTTAAAATTCTAACTCGAC

Sequence ID - 911   nt: 595
GAGGGTGTAGAAGAGAAGAAGAAGGAGGTTCCTGCTGTGCCANAAACCCTTAAGAA
AAAGCGAAGGAATTTCGCAGAGCTGAAGATCAAGCGCCTGAGAAAGAAGTTTGCCC
AAAAGATGCTTCGAAAGGCAAGGAGGAAGCTTATCTATGAAAAANCAAAGCACTAT
CACAAGGAATATAGGCAGATGTACAAANCTGAAATTCGAATGGCGAGGATGGCAAG
AAAAGCTGGCAACTTCTATGTACCTGCAGAACCCAAATTGGCGTTTGTCATCAGAA
TCAGAGGTATCAATGGAGTGAGCCCAAAGGTTCGAAAGGTGTTGCAGCTTCTTCGC
CTTCGTCAAATCTTCAATGGAACCTTTGTGAAGCTCAACAAGGCTTCGATTAACAT
GCTGAGGATTGTAGAGCCATATATTGCATGGGGGTACCCCAATCTGAAGTCAGTAA
ATGAACTAATCTACAAGCGTGGTTATGGCAAAATCAATAAGAAGCGAATTGCTTTG
ACAGATAACGCTTTGATTGCTCGATCTCTTGGTAAATACNGCATCATCTGCATGGA
GGATTTGATTCATGAGATCTATACTGTTGGAAAAC

Sequence ID - 912   nt: 651
CATTTCCAGAGTTTATGTGAATTGAATTGAACTATGGTTTTATGTTACTGTCAGTA
GAATGAAGTACGAATATTTGAAAAATACACCTTCAACTTCAAAGTGATTCTTGACA
AAAATTATAAGGAATCATTTTGGACACATTTTCTGGTAGAGCCTTGTAAAAATTAA
AACCAAGTGTTGTTTTCAAGAAGAACTGTAATACATAATCAGGAATTTGAGTAGGG
AGATTATTTTGTTATTTAAAATTAAAGTGGCTGTGTAGTTTTAACTTTAGTATTGC
AGGTAGAGTAAGCTTACATGATAACAAAAATCTTGGTCTTAGTGACTTAATGATTC
TGATATTTATTGATTGATTGGTTATCATTCCAAATATTTTAAAAGATAATAGCTGG
CTGGGTGCGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCAGGACGGGCG
GATCACGAGGTCAGGAGATCAAGACCATCCTGGCTAACACGGTGAAACCCCGTCTC
TACTAAAAATCAAAAAATTAGCCGGGTGTAGTGGCGGGCACCTGTAGTCCCAGCTA
CTCAGGAGGCTGAGGCAGGAGAATGGCATGAACCTGGGAGGCGGAGCTTGCAGTGA
GCTGAAATCGTGCCACTGCCTCCACCTGGCGACAA

Sequence ID 913
GTGAGGTGGGGACTTCATTCATTGTCCTATTTCTATCTCCACTTTGTGCCTGGAGA
GCTTTCAGGGGAGGTGGAGGAGGAGGGTCTGCCAAGCTACTGCAACATCTGTCACC

CACTATACCCAGTTACTTGGGGGAGGACAGACACTGTGGTGTCATTAAAGTTGTTT
GAACCAAAGTGGCGGCTGCATCTTTGTCCCGATGCTAGCCGTGCCGGTCTCCCATC
ATCCGCTCGCCCTCCTTTNCCCTGGGCTGCGCCCACTTGTCTTCCTGGATATTTGG
GGGTGACTCGCCATGCTTGGCACCCTCTGCTTCCTGGTGCTGCTCTGACTCGAAGA
CGGACAGTCCCTGGTGCACATCCAGGGAAGAGGAGTGTCGGTAGTTCTTGCAGTA
GGCACTTTATCAGGACCTGACCTGTTGCTGGGTGATTTTAGTCTCTACAAACAGAA
AGCGTTTCAAAGCGTCAGCTGTGGGAGCAGAGTGACCCTTTGCTGATGCTGGGGGG
AGGGGATCTAAATCCTCATTTATCTCT

Sequence ID 914

GGCGCCTGCTGGAGGAGGAGAGAGCTCTGCTGGCATGAGCCACAGTTTCTTGACTG
GAGGCCATCAACCCTCTTGGTTGAGGCCTTGTTCTGAGCCCTGACATGTGCTTGGG
CACTGGTGGGCCTGGGCTTCTGAGGTGGCCTCCTGCCCTGATCAGGGACCCTCCCC
GCTTTCCTGGGCCTCTCAGTTGAACAAAGCAGCAAAACAAAGGCAGTTTTATATGA
AAGATTANAAGCCTGGAATAATCAGGCTTTTTAAATGATGTAATTCCCACTGTAAT
AGCATAGGGATTTTGGAAGCAGCTGCTGGTGGCTTGGGACATCAGTGGGGCCAAGG
GTTCTCTGTCCCTGGTTCAACTGTGATTTGGCTTTCCCGTGTCTTTCCTGGTGATG
CCTTGTTTGGGGTTCTGTGGGTTTGGGTGGGAAGAGGGCCATCTGCCTGAATGTAA
CCTGCTAGCTCTCCGAAGCCCTGCGGGCCTGCTTGTGTGAACCGTGTGGACAGTGG
TGGCCGCGCTGTGCCTGCTCGTGTTGCCTACATGTCCCTGGCTGTTGAGGCGCTGC
TTTAACCTGCACCCCTNCCTTG-CTCATANATGCTCCTTTTGA

Sequence ID - 915   nt: 230
TTTGAGACCAGCCTAGCCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAAA
TTAGCCGGGCGTGGCGGCACATGCCTATAATCCCACTTACTTGGGAGGCTGANGTA
GGAGAATCGCTTGAACCCANANAGGCAGAGTTTGCAGTGAGCCGAGATTGTGCCAT
TGCACTCCAGCCTGGGCGACAGAGCGAGACTCCATCTAAAANAAAATAAATGAATA
AAATAA

Sequence ID 917
NNCAGATTTTTTTTTTTTTTTCAGNGTTAGACCATCTTTCAATTCCTGGAACAAAC
TTAACTTTCCATGATATGTATTTTTTATACATTGCTGGATTTTATTTGCTAATATT
TTACTTAGGATTTAATTTTCTAAGTNGACCTATAATTNTCCTGTATAAAATTGCAT
TTGTCACATTTTAGTATCAAGGTTGTCCTANCNCCATGAAATGGATTTANAATGGT
TTATGTAANATAAAGTACATTTCTTCTAAAGGTTTGNGTGGATTAACTTTCAAATC
TGCCANAGNGNGTTTTTTTCCTTTTTTTTTTTTTTTTCATTTNAAGGGAGNGCAAGT
ANCTTTTCAAATNCTGATTTAATTTTTAAAATATTTNCAAGTNTNTTTANAGTTTT

- 236 -

TATTTNTTNTNGAANGTTAACATTTTTATANAAAANGGTNTTATCTTTTTAAATTC
TTTGACATCAGTTTCTTCANAATTCCTTCTTTTAA

Sequence ID 926

GTCATATCTCTTCCCAGGGAAAGCAGGAGCCCTTCTGGAGCCCTTCAGCAGGGTCA
GGGCCCCTCGTCTTCCCCTCCTTTCCCAGAGCCATCTTCCCAGTCCACCATCCCCA
TCGTGGGCATTGTTGCTGGCCTGGCTGTCCTAGCAGTTGTGGTCATCGGAGCTGTG
GTCGCTACTGTGATGTGTAGGAGGAAGAGCTCAGGTAGGGAAGGGGTGAGGGGTGG
GGTCTGGGTTTTCTTGTCCCACTGGGGGTTTCAAGCCCCAGGTAGAAGTGTTCCCT
GCCTCATTACTGGGAAGCAGCATCCACACAGGGGCTAACGCAGCCTGGGACCCTGT
GTGCCAGCACTTACTCTTTTGTGCAGCACATGTGACAATGAAGGACGGATGTATCA
CCTTGATGGTTGTGGTGTTGGGGTCCTGATTTCAGCATTCATGAGTCAGGGGAAGG
TCCCTGCTAAGGACAGACCTTAGGAGGGCAGTTGGTCCAGGACCCACACTTGCTTT
CCTCGTGTTTCCTGATCCTGCCTTGGGTCTGTAG

Sequence ID 938

TGGCCATCCTTTTCCCCCCAAACACACCCCCTTAACCTATCTCTTGGGACTTAGCC
CGACCCTCCCTCTCATTTCCCATTAAGTCTGAGAGGCAAGAGCTAGGTTAGGCAAG
GAGGTGGTTGGCCAGAGATGGGGAACAGCCAGGTGCCCCAGTCCTCTGATTTTTCC
TCCATCCTGCTTACCACCTCCCTGGGTACTTACAGCCTTCTCTTGGGAACAGCCGG
GGCCAGGACTGGGTCACCTATGAGCTGAATCAGCATCTCCTCCTGAGTCCCAGGGC
CCCTGCAGTTCCCAGTCTCTTCTGTCCTGCAGCCCTTGCCTCTTTCCCACAGGTTC
CACTTTATATCCACCTTTTCCTTTTGTTCAATTTTTATTTTTATTTTTTTTATTAT
TAAATGATGTGGTCTATGGAAAAAAAAATAAAAATCTGACTTAGTTTT

Sequence ID - 939   nt: 513

GGAACCCAGTGTATTACCTGCTGGAACCAAGGAAACTAACAATGTAGGTTACTAGT
GAATACCCCAATGGTTTCTCCAATTATGCCCATGCCACCAAAACAATAAAACAAAA
TTCTCTAACACTGCAAAGAGTGAGCCATGCCTGTTAACACTGTAAAGAATGTAACA
TGTGGGGACACACAGGGGCAGATGGGATGGTTTAGTTTAGGATTTTATTAGTGCA
TGCCCTACCCTCTGGGGGAACGTCCCATCTGAGGTTTTCTTCTCGGTGGGGGGATT
TAACTTCTGTCCTAGGGAAAACAGTGTCTGATGAGGAGTGTTTCCAACACAGGCTA
CATGAATTCCCCTATACCAGTGCGAAAGCAGCCAGGAGTCCCCGTTGGAAAAGAAC
AATGCCACTCTCTTTTATGTATCTTGGTTCTGCAACTCATTTGTTGTAAGTAGGGT
TAATCGAGTATCAGGTTCACAGTATCCTGCCCTTATTATTTTATGATTCACTGACT
CAAGTTCCA

Sequence ID 947

GAGAGTGAAAAAATTCTGGTACAAATTGGGAAATTAGTATATAACAACATAGTGTT

AAATTCAATGGGAAAAGTTTAATAAGAGGATTTGGTATCAACTGGCTGTCCAAAGA

TAAAAATGGACCGTCCTATCACATACAAAATTGTTTTTTAGATAAAGATTTAAATA

CAGGCACTCCTTCATTTGCGTGGTGCACCTTGAGGTGTTGCAGAAATGATGAGAGC

TGAAACTGCAAAGCAATTTTAATACTTTATCTGTTGGAAATCTTATAGTTTTCCTG

TGACCGTTAAAATTTTCATTAAACTATTAAAAACACCCATGACTGGTCACAAATGT

ATTGGGAAATGGAAAGAATTAATACACTAAAAATACAAAAAATAGAAAATATTTA

AAATTATCTAAAAATTTGAAACATTAGAAAAATTGAGAACTAGGCAGGGCGTGGTG

GCTCACATCTGTAATTTTAGCCCTTTGGGAGGCTGANGCAGGTGGATCACCTGANG

TCAGGAGTTCGAGACCAGCCTGCCAACGTGGGGAAACCCCGTCTCTACTGAAAATA

CAAAAATTANCCGGGCATGGTGGCACAAGCCTGTAATNCTTGCTNACCAGGANGCT

GAGGCAGGAGAATCACTTGAACCCANGANG

Sequence ID 949

GTTTCACATGAGAAGGTAGTATTATGTACAGTGACCTTGTTTAAAGTGTCNGTTTA

ATGTTACCACTAAGGCCCTGCCCCAGCTTTATCACCTGAGCACTAACAAGTGCTGT

GTGGAGTTCAGTCCATGCTGGTAACTNTTGAGTATTCAGTGGGTCTTTTAACAATT

ACCACCGTGGAGGANANAGCAAGGAAGAGAAATGCTGTGATCTTTTNCTGTTTTTA

ATTAGNGAAAGAGGGATTANATTAAACAAATGTTACAGAGNTGTGACTNTGATCCC

CCAGNGGTAAGCAATAATTGTANAGACTGGATTTNANAAGCCCTGAGAGTTTATTT

TCAACCTATNTATTATAGNNCAATCC

Sequence ID 1028

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ATGGGGTCAAGGCACCAGGACTGA

Sequence ID - 1056   nt: 435

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ACACCTCTCCTTTGTGACTTCAAGAGCCTCTGGCATCTCTTTCTGCAAAGGCATCT

GAATGTGTCTGCGTTCCTGTTAGCATAATGTGAGGAGGTGGAGAGACAGCCCACCC

CCGTGTCCACCGTGACCCCTGTCCCCACACTGACCTGTGTTCCCTCCCCGATCATC

TTTCCTGTTCCAGAGAAGTGGGCTGGATGTCTCCATCTCTGTCTCAACTTCATGGT

GCGCTGAGCTGCAACTTCTTACTTCCCTAATGAAGTTAAGAACCTGAATATAAATT

TGTTTTCTCAAATATTTGCTATGAAGGGTTGATGGATTAATTAAATAAGTCAATTC

CTGGAAGTTGAGAGAGCAAATAAAGACCTGAGAACCTTCCAGA

- 238 -

Sequence ID 1071

NGATATAGTNCCGCATGGGAAAGATGANCAGGTATAACCNAGCNTNATATAGCAAG
GACTAACCCCCCTGCCTTCTGCATAATGAATTAACTAGAAATAACTTNGCAAGGAG
AGCCAAAGCTAAGACCCCNGAAACCAGACGAGCTACCTAAGAACAGNTAAAAGAGC

5   ACACCCGTCTATGTAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCT
ACCGAGCCTGGTGATAGCTGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATT
NGCCCACAGAACCCTCTAAATCCCCTTGTAAATTTAACTGTTAGTCCAAAGAGGAA
CAGCTCTTTGGACACTAGGAAAAAACCTTGTAGAGAGTAAAAAATTTAACACCC
ATAGTAGGCCTAAAAGCAGCCACCAATTAAGAAAGCGTTCAAGCTCAACACCCACT

10   ACCTAAAAAATCCCAAACATATAACTGAACTCCTNACACCCAATTGGACCAATCTA
TCACCCTATAGAAGAACTAATGTTAGTATAAGTAACATGAAAACATTCTCCTCCGC
ATAAGCCTGCN

Sequence ID - 1074   nt: 689

15   GGGAGGCGGAGGCTGCAGTGAGCTGAGATCGTGCCACTTCATTCCAGCCTGGGCAA
CAAAGCGAAACTCTGTCTCAAAAAAAAAAAAAAAAAAAATTTGTTGACTGTTGTAA
TTTAAAGCTTGTCATTTTTTATTTAGTAATAACACTCATTAGTGTAGTATCTATGA
TGAACCAGGTTCTGCACAAAGTACCTTATGTTCATGGCCTCATATCGTCTTCTCCA
AAACTCTGCAAGATAGGATTCATCACCACTTATAGGGAGAGATCTGAAAGTTTAAA

20   ATTGTACCCAAGGTCACACAGCTGGTAAGTGCCAGAGCTGGGATTCCGTAGGGTGT
TCANAGTGCCTCTCCTGCCGTAGGCTTATCACAAAAAGTCAAAGTTTGGTCATAAT
AAAGCCTGAAGTTTGGCAGGATTTAAAAATAGTCACCANACTTTTGAGTTGGAGCA
TCCCACCTCACTGCTGTTCACCTTCTGTGGCAGGGAGAGTCATCATTTCCATTTCA
GCTTGTGGAATATCTTGTCATTAACATTCTCATGCAAAAGCCATTTTATGGTGCCC

25   AATGAANATGGTTAAGCTACTGCCCCAAGCCTNTGGAAGCCTTCCTAATTTTGGAC
TTGCACTATGCAAATTGNATAATATTTTCTACCCTAAGCCAAATATTTTCTTCA
CTTTTCATTCATTCTAC

Sequence ID 1081

30   CGCCGCCGCGCCGCCGTCGCTCTCCAACGCCAGCGCCGCCTCTCGCTCGCCGAGCT
CCAGCCGAAGGAGAAGGGGGGTAAGTAAGGAGGTCTCTGTACCATGGCTCGTACAA
AGCAGACTGCCCGCAAATCGACCGGTGGTAAAGCACCCAGGAAGCAACTGGCTACA
AAAGCCGCTCGCAAGAGTGCGCCCTCTACTGGAGGGGTGAAGAAACCTCATCGTTA
CAGGCCTGGTACTGTGGCGCTCCGTGAAATTAGACGTTATCAGAAGTCCACTGAAC

35   TTCTGATTCGCAAACTTCCCTTCCAGCGTCTGGTGCGAGAAATTGCTCAGGACTTT
AAAACAGATCTGCGCTTCCAGAGCGCANCTATCGGTGCTTTGCAGGAGGCAAGTGA
GGCCTATCTGGTTGGCCTTTTTGAAGACACCAACCTGTGTGCTATCCATGCCAAAC

- 239 -

GTGTAACAATTATGCCAAAAGACATCCAGCTAGCACGCCGCATACGTGGAGAACGT
GCTTAAGAATCCACTATGATGGGAAACATTTCATTCTC

Sequence ID - 1083   nt: 198
GCGCGTCGACTTTGTTTAGACATTGAATGACTTTGTTAAAGGCACAATTAATCACA
TTGGTTGTACTCTGNNGACAGCCTTCTTTAAAAAAAAAATAAACAATTTAAAACAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAANTTTTAACC

Sequence ID - 1084   nt: 198
GCGCGTCGACTTTGTTTAGACATTGAATGACTTTGTTAAAGGCACAATTAATCACA
TTGGTTGTACTCTGNNGACAGCCTTCTTTAAAAAAAAAATAAACAATTTAAAACAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAANTTTTAACC

Sequence ID - 1099   nt: 561
TGCATGCTTGTGGATTGGAAAAACTTTGGAGACTGATTACTTTTCATTATATATGT
GTCACAGTGAAACAGCTTTTATGTGTCATGTAAGATTACTGCTTGCCTCTCTAAGG
AAGGTCGTGACTGTTTAAATAGACGGGCAAGGTGGAACCTTTTGAAAGATGAGCTT
TTGAATATAAGTTGTCTGCTAGATCATGGTTTGTATTGAACTAACAAGGTTTGCAG
ATCTGCTGACTTATATAAAGCTTTTTGATTCCTACTAAGCTTTAAGATTTAAAAAA
TGTTCAATGTTGAAATTTCTGTGGGGCTCTATTTTTGCTTTGGCTTTCTGGTGAGA
GAGTGAGGAAGCATTCTTTCCTTCACTAAGTTTGTCTTTCTTGTCTTCTGGATAGA
TTGATTTTAAGAGACTAAGGGAATTTACAAACTAAAGATTTTAGTCATCTGGTGGA
AAAGGAGACTTTAAGATTGTTTAGGGCTGGGCGGGGTGACTCACATCTGTAATCCC
AGCACTTTGGGAGGCCAAGGCAGGCAGAACACTTGAAGGAGTTCAAGACCAGCGTG
G

Sequence ID 1109
TTTGNCGGTNTTGGANNNNNANAANTTTCTTCCANNCNTNACNTNTTGGTGGNCTA
AATTAANATGGNTTTNGNGGGTTCNTTNCTNNNTNNNNCATGGGANANAATTNATT
NTCNTNCNNNTTCCTTNNCCCTNAANCTACCTTCCCCCNATTTTCTCCCCTNTTCN
TNAATTANCATCCTCTCCNCNTANNTCNANACNTTAATGGCAANACTATCTAATAN
CNANNATAANANCTCCTGTNNNCCACATNTCTTATTNNNCGCNNCANGTTNCANNC
CCNCAGAGTNAACTCATCCTCNNCNNAANTTCATATCGTGNNCTNTNNNCNNTNGC
GCGANATATTAANNANACCNGTANNTNNNANACANNANNTNNGNAANAANCCTTCT
NANNTTTTAGCNTCNNGCNNTAACNNNNNTCTTNGTGNNNNCNCAGCTTTCNCNNC

- 240 -

ATNATNCTNCNNCGAANTNTCANNCNTCTCCNCTTNAATGNNTTCCCATGNATTAA
NTNCCTCGNNNANAGCACTATCGTNNNNGAGNNNATTATNGNCNNTTTACNTCATG
TGGTCCANTNNCGTTNGNCGCNNNNAATNTTCGTNNNNCNN

Sequence ID 1118

GGATTTTAGAGGAAGGCGCTNGGTTACATTGGAGAACTGGAGTGGTCTGGAGTTCC
ACGGTGTAGTGGACCAGAGGCCACCTCTCCTGGGCTTCTCAGTGTCTCGCCGGCGG
GGTTCGGCCTGAGCTGGATTGACATAGCCCTTGGCGGATTTAAACAACCTAAACAT
TAAGCAGTACAGCTGCCTCAAACCTTTGGGATTTTCAGAATGACTGACACTGCCGA
AGCTGTTCCAAAGTTTGAAGAGATGTTTGCTAGTAGATTCACAGAAAATGACAAGG
AGTATCAGGAATACCTGAAACGCCCTCCTGAGTCTCCTCCAATTGTTGAGGAATGG
AATAGCANAGCTGGTGGGAACCAAAGAAACAGAGGCAATCGGTTGCAAGACAACAG
ACAGTTCAGAGGCAGGGACAACAGATGGGGGTGGCCAAGTGACAATCGATCCAATC
AGTGGCATGGACGATCCTGGGGTAACAACTACCCGCAACACAGACAAGAACCTTAC
TATCCCCAGCAATATGGACATTATGGTTACAACCAGCGGCCTCCTTACGGTTACTA
CTGATAGAAATGTTGGCAGCTTTTAGTAAAAGCATTTACTCTGTTACCATGAGAAA

Sequence ID 1125

NGACTGGCTCCCGAAAAGAAGGGTGGCGAGAANAAAAAGGGCCGTTCTGCCATGGA
CGAAGTGGTAACCCGCGAATACACCATCAACATTNACAAGCGCATCCATGGAGTGG
GCTTCAAGAANCGTGCACCTCGGGCACTCAAAGAGATTCGGAAATTTGCCATGAAG
GAGATGGGAACTCCATATGTGCGCATTGACACCAGGCTCAACAAANCTGTCTGGGC
CAAAGGAATAAGGAATGTGCCATACCGAATCCGTGTGCGGCTGTCCANAAAACGTA
ATGAGGATGAAGATTCACCAAATAAGCTNTATACTTTGGTTACCTATGTACCTGTT
ACCACTTTCAAAAATCTACAGACAGTCAATGTGGATGANAACNAATCGCTGATCGT
CAGATCAAANAAANT

Sequence ID - 1139   nt: 503

CAGCACTGCCAGTGGAGATGGGCGTCACTACTGCTACCCTCATTTCACCTGCGCTG
TGGACACTGAGAACATCCGCCGTGTGTTCAACGACTGCCGTGACATCATTCAGCGC
ATGCACCTTCGTCAGTACGAGCTGCTCTAAGAAGGGAACCCCCAAATTTAATTAAA
GCCTTAAGCACAATTAATTAAAAGTGAAACGTAATTGTACAAGCAGTTAATCACCC
ACCATAGGGCATGATTAACAAAGCAACCTTTCCCTTCCCCCGAGTGATTTTGCGAA
ACCCCCTTTTCCCTTCAGCTTGCTTAGATGTTCCAAATTTAGAAAGCTTAAGGCGG
CCTACAGAAAAAGGAAAAAAGGCCACAAAAGTTCCCTCTCACTTTCAGTAAAAATA
AATAAAACAGCAGCAGCAAACAAATAAAATGAAATAAAAGAAACAAATGAAATAAA
TATTGTGTTGTGCAGCATTAAAAAAAAATCAAAATAAAAATTAAATGTGAGCAAAG

Sequence ID - 1148   nt: 587

TGAAAAATAAAGTTTTTATGTATATTCTACATATGTATATGTTGGTAGAAAGCAAA
AACGCTAGGTAAAAATAAATGTAATACAATTTTAGCTATGAACCAAAAAACCATTT
GTGGTGTGGATGCAAGAAAGTCTGGATGGGTGCAGAGTTCTCCATGTTTCACTTCT
GACATTTGAAAATACGCAGTTTGCATTTGATACGTCAAATGTTATTTTTAAGAAAA
CCAATAAAATCATTAAAACCGAAAAGGCAGTTTTGCTTGTTTTTACCTTAGTTGGA
GTTATCTGCAATTGCCGTATTAGTGTTTTAAGGAACTTGTAAGTAAGCTCCTTAGT
CCCCTTTAGAGCTACGAAACATGTCAATTTTACTTTTCTCCAGCTTTTTGGAATCT
TATCTAAATTACCATGTAGAGTTCTGCATAGCTTCAAATTCTCTTAGCCAATGTGG
TCTGTAAGTGTCTATCGATGAATTTCACCGTTAATTGCCGTAGTATACTGTCCTGT
ACCGGATGTGAAGAGGAGCAACTCTGCACAGTGCACTGGTTGCTCCCATGGTAGGA
ANGAATGGCTTATCAATGGTCGGATTT

Sequence ID - 1160   nt: 650

GGAGGATGGAGCAGTGAGCGGGTCTGGGCGGCTGCTGGCAGCGCCATGGAGACGGT
ACAGCTGAGGAACCCGCCGCGCCGGCAGCTGAAAAAGTTGGATGAAGATAGTTTAA
CCAAACAACCAGAAGAAGTATTTGATGTCTTAGAGAAACTTGGAGAAGGGTGAGTG
TAAAGAAACTATAGGTAGGTCATTGGGTCCCAGTCTTTTTCCTGCCCCAGAAGAAG
CAGAAGGATATGAACCTTTCAGCATTGTTCTAGGTGGGGTGGAAGGTAAATTTACA
GCTTGTGATGTCCTTCTTCGCTTTACTCCAATCCCTATTATAGACAGATTTAGTGA
TTCCTGGTCTTTTTAACACGAAGAATATCTATTGTTTTCTCTTTTGTAGGATCTGT
ATGATTTTATCTACTTAACAGATAGCACTAATTAGATTAAAATTCTATAAGAAACT
TTTTAATTTGCTGTTCATAATTTCTGATTGGTATGCAATAACTGTTTCAATGAAAA
TCAATGTAATTTAGTATTTTAATATTTGCACCTTTGTGAAATATAGTAAATAAATT
AAGCACTATCACCACCTTCACAGCTACTTAGGAGATCCACAATCCTGGGTTGGGAG
CCAGTGGATTTCCTGAAACACAGATTTGTTAATG

Sequence ID - 1165   nt: 502

CTCAAGTGAATCCTGGCTTCTTGGAAGCGCTTGCCTAGACGAGACACAGTGCATAA
AAACAACTTTTGGGGGACAGGTATGTTTTCTTGCAGCTGCGGTTGTAAGGTCTTGG
CAAGACAAGCAGTGTGGCCAGAATTTTGAACTTCTGATGAATGTGTAATGCAAAGG
ACCTTGTACATTTTTTTGTTTCAAGGTCCTCAAAATGAGCACATGAAGAGGTTGCT
GTGAAACTTTAAGTGGCCCTACTGCGCAGAAGCATTCAGATGTCACTTGATGATCT
GTAAGGGAACTTGCTGATTTGGGAATGTGCTTAGGGAACACACATTCCTTTTGACA
GGGTCTGTCACTGGGTGGGTGATGAATTATACAGATGACATGTGCTTTTTTTTCTT
TTTTCAACCTCAATGGTATTCCTACAGGAAATGGATAACCATTTTAACTGTATTTT
TTGCAGCCCGTACCTTCTTGGGAATACAATTGTCTAACTTTTTATTTTTGGTCT

Sequence ID - 1172

nt: 648

CCACAATAATAAGAGAAAAACAGGAGCAAAAGGATATACAAAACCACCAGAAAACA
AATAACAAAGTGACAGGAGTAAGTCCTTAACTGGCAATAATAACCATGAATCTAAA
TGGATTCCATTTCCCACTTAAAAGATAAAGACATGCTGAATGGATAAAAAGCTGTC
ACCCAGTTATATGCTGCCTACAACAAACTCACTTCACCTGTAAACATACATATGGA
TGGAAAGAGAAGGCATGGGAAAAGATACTCTACTCAAATGAAAACAAAAACCAAAC
AACACAAAGTCATTGTATAATGATGAATTCAATTATATCATGATGAATTCAATTAT
ACCCAACACCAGAGCATATAAATATGTAAAGGAAGATAAAGGGAGTCCTGTGATCA
AGAATAAATATAACAATTATAAATATTTTATCTAAAGTGATAGATAGACTGTAATA
CAATAATAGGGTGGTGACATTAACACCCCCTCTCACATTGGACTGATCATCTAGAA
GGGAGAAAAGCTTTATGATTGGAAAAGCCAT

Sequence ID 1178

ATTGTGTTGGCCACCCGGGAATTCGCGGCCGCGTCGACCTACGCACACGAGAACAT
GCCTCTCGCAAAGGATCTCCTTCATCCCTCTCCAGAAGAGGAGAAGAGGAAACACA
AGAAGAAACGCCTGGTGCAGAGCCCCAATTCCTACTTCATGGATGTGAAATGCCCA
GGTGAGGAGACGGCTTGCTGTAGTGGGGAAAGCACTGGACCTCAACAGTTGGAAAA
TGTTGTAGTGTTAGCTGTCTCGTATCCTTGAAGCTGTGCAGCAGCTTCAGTTTCTT
CGCCTGTGGAAAATATTTTCCCTGATACTCTTAAAATTTGAATGTATGAGACTGGC
AAAGTTTTGCATCTTAGGAGGAGTGATTCATTTCACCGTGATCTCTCATCACATTT
CACATACAACCCCTACGTTTTTTTGTGTTGGGAAACAATGTAATGGATGATGAGTT
GGGCATAAGTGCAGGAAAGACGGGTGTAATAGAGGAAAAAAATGTTATCTGCTTTT
CTTTCAGGATGCTATAAAATCACCACGGTCTTTAGCCATGCACAAACGGTAGTTTT
GTGTGTTGGCTGCTCCACTGTCCTCTGCCAGCCTACAGGAGGAAAAGCAAGGCTTA
CAGAAGGATGTTCCTTCAGGAGGAAGCAGCACTAAAAGCACTCTGAGTCAANATGA
GTGGGAAACCATCTCAATAAACACATTTTGGAT

Sequence ID - 1180

nt: 622

CTTTTCCTCCCGCTGTCCCCCACGGGAGGGGACTGCTCTCCCCCGCTGCATCCTTT
CTGTGAGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCT
CGACATTCGGGAAGTGTTTTTGAGAAGTCTCGGTCGGTAAGGGAAGTCTTCCAAGT
CCGTGCAGCACTAACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCCAGATGAG
GCAGCTGTGACTGTGTCAAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCT
TCCACTGCCGTCTCCACAGGAAACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCA
TCAAGGCATTTATTGCAGTGTACTATTTGCTTCCAAAGGATCAGGCCCTGAGAACA

- 243 -

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ATGACCTTATTTCCTACAACAGTGTCTGGGTTGCGTGCCAGCAGATGCCTCAGATA
CCAAGAGATAACAAAGCTGCAGCTCTTTTGATGCTGACCAAGAATGTGGATTTTGT
GAAGGATGCACATGAAGAAATGGAGCAGGCTGTGGAAGAATGTGACCCTTACTCTG
GCCTCTTGAATGATACTGAGGAGAACAACTCTGACANCCACAATCATGAGGATGAT
GTGTTG
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Sequence ID - 1181   nt: 155
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CGCCACTTATCCAGTGAACCACTATCACGAAAAAAACTCTACCTCTCTATACTAAT
CTCCCTACAAATCTCCTTAATTATAACATTCACAGCCACAGAACTAATCATATTAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
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10

Sequence ID 1182
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CATTGTGTTGGCNCCCGGGAATTCGCGGCCGCGTCGACTTTTTGTGTTGTTTGGAG
CAGAAATACTAAAGAAGATTCCGGGCCGAGTATCCACAGAAGTGGACGCAAGGCTC
TCCTTTGATAAAGATGCGATGGTGGCCAGAGCCAGGCGGCTCATCGAGCTCTACAA
GGAAGCTGGGATCAGCAAGGACCGAATTCTTATAAAGCTGTCATCAACCTGGGAAG
GAATTCAGGCTGGAAAGGAGCTCGAGGAGCAGCACGGCATCCACTGCAACATGACG
TTACTCTTCTCCTTCGCCCAGGCTGTGGCCTGTGCCGAGGCGGGTGTGACCCTCAT
CTCCCCATTTGTTGGGCGCATCCTTGATTGGCATGTGGCAAACACCGACAAGAAAT
CCTATGAGCCCCTGGAAGACCCTGGGGTAAAGAGTGTCACTAAAATCTACAACTAC
TACAAGAAGTTTAGCTACAAAACCATTGTCATGGGCGCCTCCTTCCGCAACACGGG
CGAGATCAAAGCACTGGCCGGCTGTGACTTCCTCACCATCTCACCCAAGCTCCTGG
GAGAGCTGCTGCAGGACAACGCCAAGCTGGTGCCTGTGCTCTCAGCCAAGGCGGCC
CAAGCCAGTGACCTGGAAAAAATCCACCTGGATGAGAAGTCTTTCCGTTGGTTGCA
CAACGAGGACCAGATGGCTGTGGAGAAG
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Sequence ID - 1183   nt: 479
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CGTGGCAGCCATCTCCTTCTCGGCATCATGGCCGCCCTCAGACCCCTTGTGAAGCC
CAAGATCGTCAAAAAGAGAACCAAGAAGTTCATCCGGCACCAGTCAGACCGATATG
TCAAAATTAAGCGTAACTGGCGGAAACCCAGAGGCATTGACAACAGGGTTCGTAGA
AGATTCAAGGGCCAGATCTTGATGCCCAACATTGGTTATGGAAGCAACAAAAAAAC
AAAGCACATGCTGCCCAGTGGCTTCCGGAAGTTCCTGGTCCACAACGTCAAGGAGC
TGGAAGTGCTGCTGATGTGCAACAAATCTTACTGTGCCGAGATCGCTCACAATGTT
TCCTCCAAGAACCGCAAAGCCATCGTGGAAAGAGCTGCCCAACTGGCCATCAGAGT
CACCAACCCCAATGCCAGGCTGCGCAGTGAAGAAAATGAGTAGGCAGCTCATGTGC
ACGTTTTCTGTTTAAATAAATGTAAAAACTG
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Sequence ID - 1185   nt: 628
CTTTGATTACCTTTGAGTATTAGGTTGAAAGCTTCTCTGTGCTTGATTGAACATTG
TGATGATGTTGATTGGGTCATGTCAGATTTAGACAGTGTTGTGTTTAAGATAAATG
TTTAATGGCTCTTAGCAGTGTTCATGCCTCCCCTTTTCCCCTGATACTTTAAAAAC
5   AGAATATACAGAAAGGGGAGTTGGGTGAAGAATCACCATATTCTCATTACCAGAG
TAGTGTCTACCAGCTGTTTTCACATTTTTCTGTTTCCTTCTGTCCTTGGAATCCTT
TTTTTAGATCCTTGTAATACTAGTAAAGATATTCCACTCTGTGTTGTAAGCATTTT
TCCATTTTGCTCCATGGTCTTCATAATGCCCTGTGGTCCTTTATTAAGGGGATGCA
CCATGTAGAGGTGAAAGGCTTTCCTTGACTTGGCCACCATTTCTGTATTTTCCTTA
10   GAGGAGGAGGTTCCAACATTTCTTTTTTAGAGACAGAGTCTCGTTCTGACACGCA
GGCAGGAGTGCAGTGGCATGATAACAGCTCACTGCAGCCTCGAACTCCTGGGCTCA
AGTTATCCTCCCACCTCAGCTTCCTGAGTAGCTAGGACTGCAGGTGCCTGCCACCA
CACCCAGCTAAT

15   Sequence ID - 1186   nt: 494
CAGCCCTCCGTCACCTCTTCACCGCACCCTCGGACTGCCCCAAGGCCCCCGCCGCC
GCCTCCAGCGCCGCGCAGCCACCGCCGCCGCCGCCTCTCCTTAGTCGCCGCCA
TGACGACCGCGTCCACCTCGCAGGTGCGCCAGAACTACCACCAGGACTCAGAGGCC
GCCATCAACCGCCAGATCAACCTGGAGCTCTACGCCTCCTACGTTTACCTGTCCAT
20   GTCTTACTACTTTGACCGCGATGATGTGGCTTTGAAGAACTTTGCCAAATACTTTC
TTCACCAATCTCATGAGGAGAGGGGAACATGCTGAGAAACTGATGAAGCTGCAGAA
CCAACGAGGGTGGCCGAATCTTCCTTCAGGATATCAAGAAACCAGACTGTGATGAC
TGGGAGAGCGGGCTGAATGCAATGGAGTGTGCATTACATTTGGAAAAAAATGTGAA
TCAGTCACTACTGGAACTGCACAAACTGGCCACTGACAAAAATGAC
25

Sequence ID - 1188   nt: 599
GGGAGACAAGCCCAGCCTTTCGGCGAGNATACGTCTAACCCTGTGCAACAGCCACT
ACATTACTTCAAACTGAGATCCTTCCTTTTGAGGGAGCAAGTCCTTCCCTTTCATT
TTTTCCAGTCTTCCTCCCTGTGTATTCATTCTCATGATTATTATTTTAGTGGGGGC
30   GGGGTGGGAAAGATTACTTTTTCTTTATGTGTTTGACGGGAAACAAAACTAGGTAA
AATCTACAGTACACCACAAGGGTCACAATACTGTTGTGCGCACATCGCGGTAGGGC
GTGGAAAGGGGCAGGCCANAGCTACCCGCAGAGTTCTCAGAATCATGCTGAGAGAG
CTGGAGGCACCCATGCCATCTCAACCTCTTCCCCGCCCGTTTTACAAAGGGGGAGG
CTAAAGCCCAGAGACAGCTTGATCAAAGGCACACAGCAAGTCAGGGTTGGAGCAGT
35   AGCTGGAGGGACCTTGTCTCCCAGCTCAGGGCTCTTTCCTCCACACCATTCAGGTC
TTTCTTTCCGAGGCCCCTGTCTCAGGGTGAGGTGCTTGAGTCTCCAACGGCAAGGG
AACAAGTACTTCTTGATACCTGGGATACTGTGCCCAGAG

Sequence ID 1189

GGGAGACAAGCCCAGCCTTTCGGCGAGATACGTCTAACCCTGTGCAACAGCCACTA
CATTACTTCAAACTGAGATCCTTCCTTTTGAGGGAGCAAGTCCTTCCCTTTCATTT
TTTCCAGTCTTCCTCCCTGTGTATTCATTCTCATGATTATTATTTTAGTGGGGGCG
GGGTGGGAAAGATTACTTTTTCTTTATGTGTTTGACGGGAAACAAAACTAGGTAAA
ATCTACAGTACACCACAAGGGTCACAATACTGTTGTGCGCACATCGCGGTAGGGCG
TGGAAAGGGGCAGGCCAGAGCTACCCGCAGAGTTCTCAGAATCATGCTGAGAGAGC
TGGAGGCACCCATGCCATCTCAACCTCTTCCCCGCCCGTTTTACAAAGGGGGAGGC
TAAAGCCCAGAGACAGCTTGATCAAAGGCACACAGCAAGTCAGGGTTGGAGCAGTA
GCTGGAGGGACCTTGTCTCCCAGCTCAGGGCTCTTTCCTCCACACCATTCAGGTCT
TTCTTTCCGAGGCCCCTGTCTCAGGGTGAGGTGCTTGAGTCTCCAACGGCAAGGGA
ACAAGTACTTCTTGATACCTGGGATACTGTGCCCAGAGCCTCGAGGAGGT

Sequence ID 1190

GTTTAAATTTGACAAACTAAAGCTNATNACTGCTATAAGAGTAATAACTGCTCATT
TTCCATAACTCATTCTTAAAGTTTTAGTAATGTAAAAGTTATTTTTTTGCAGTAAG
TTATAATGATAGAAGCTTACATGTTTTTTCATGCCTCATCTGTTTCCCCTTAAAAC
TATAATTATCAGTAAAGTCCTGTGGTATTTTTCAATTTGTAAGAAACTAGGCTATA
TATACATTGGGAAAAACAGCCTTCATTTGTCAATGCACTAGTGTTCCAAAGGTTTC
TGGTAATTGTGTGCTATTGCTTTTTGTTGACTTGCAAAAAAAAAAAAAAAAAAAATT
ACTATGACTTGNGGTAGCCCTGCAACCTTCGGAAGTGCTTAGCCCAGTCTGACCAT
ACATTTATATTTANAATGCTTAGGTAAATAAATAATATGCCTAAACCCAATGCTAT
AAGATACTATATAATATCTCATAATTTTAAAAATCACTGTTTTGTATAATAATAAA
ACAAGGCAGGCAAGCTGTTCTACAATGACTGTTGGTAAGGGTGCTGAGGAAGAAAA
ACAAACAATCTTGATTCAGGGATAGTGAATAGACAAAAAATGTCCTAATCAATGAA
GCTGTGTGATGATTCTGATTGACAGAGA

Sequence ID 1191

GTGCAAAGTGTTATATCCACTTTCAACAAAGAGAGAAGCTGAAAAGCTAACCCAAT
GTTAATTTTGGATCACACACATTCAGTGTAGACTTTAAGATTTTACTTCTGTTGGA
GTAGCTATATTATTTCTAGTTAAAAAACTCTCTATATACATATTTATTTGTTTTTC
TACTTGTTTAATATTTTTCTCTTCCAATTAGGAACTCAATATGGAATAAAAAATAT
TTAAATGTATTTTACTCAAACGTGTGTGTATATGTTTGTGTGCATGATAAGGAG
AGTGAGAGCAAGAGTAAGAGAGAGAGAGCACGCATAGATGGAAGCACACATTTAAT
GTCTATGAAATGAGAAAACATTAAGGCTAAGATATTTTCCTTCTGAACTAGCAGA
TTGTATCAATGGCTGGTCACTTAAATTAATCAGTTTGTAAAGATATTTAAAAGGTA
TGTCTACCTTCTTGCAATTAATTTGATTATGTTCTAATGGCATGGCAAGAGAAATG

AAAGAAGATAACTAAAAGTTAAAAGTCGTTGCATGTTTTTGTTGCAGCATACCCTT
CTTTCAGGCTACCGAATAACCTTGATTGACATTGGATTAGTAGTAGAATACCTCAT
TGGTAGAGCATATCGCAGCANCTACACTAGAAAACAT

5   Sequence ID 1192

GTCTGGAACTCCAGACCTCAGGTGATACCCCTGCCTCAGCCTCCCAATGTGCTGGG
ATTACAGCTGTGAAGCCACCGCGCCCGGCTGCTGTGATAGTTGAGATGTAAACCAA
AAATAAAATTCTAAGCCACCCAATCCGACTGAATGGACCCTTCCTGTTGAGCAAGG
ACATTCCAAAGTAAACTGAAAGACCAGCTTAGGCCATGATGGGAAGGGGAGGTGT
10   CAACATGCCTCATTCTACCTTCCTCCCTCTGGAATCCAGACACAACTGACCAGCAT
TAACATTAAAACAGAGATCTTAAGCTGGGCACGGTGGCTCATGCCTGTAATCCCAG
CACTTTGGGAGGCCAAGGTGGGATCACCTGAGGTCGGAAGTTCAAGACCAGCCTGG
CCGGTATGGTGAAGCCATGTCTCTACTGAAAATGCAAAATTGGCCGGACATTGTGG
TGCA

15

    Sequence ID 1193

TNCNTTTTTTTTCCCNCGGGAAAGCGCGCCATTGTGTTGGTCCCCGGGAATTCGCG
GCCGCGTCGACGAGAAATGGCTTGAACCCAGTAGGCAGAGGTTGTAGTGAGCCCAG
AATNGGNCACCTGCACNTTTANCCNTGGGTGACAAAANTGAAAACTTTGTCTNAAA
20   AAAAAAAAAAAAAAATTTTAANTNAAATNAAAAANCCTTTNCNTTNTTTTTNAAAN
NGGGGGGGGNNTTTTTNGGGNTTNGNNNTGGTAAAAANTNNNTTTTTTTTTTTTTA
GGGGCCNANNCCCCNTTTTANAAAANCCNGNTTTTNAAAAAANTTTTTTNCCCNCN
NTTNGGGGGGGGGNTTTTNANCNNTNTTNGGGGGGGGNNCCCCTNTTANNACCNNC
AAANTTTTTANTTTTTTGNNNAANNNCCCCCTTTTTTTNNTTTTTTTTTGNGGGGGGG
25   GGGNNGCCCCCNNCCTTTNGGGGGGGGGGGNTTNNGNAAAANNACTTTTNAAAANNA
AGGGNNGGGGGNANATNNCCCCCCCNGGNTTTTTTTTTTTAAAAANTNAANNGGGGG
GGGNNNCTNANTNGGGGCNCCCANNGGGGGNTTANAANNATTTTCTNCCCAAACCC
CCNGNTTTTATNNCCCCCCCCCCCCNCNNNNGAANGGGNGGNCCNTTTTTTTTTATT
TTTNNGGNGGGNAAAAAANTTTNAAAAANNANNATNTTTTTTCCCCCCCCCCCCCNC
30   TTTTNGGNAAANCCNNGGGGGGGNTCCTTTTTNAAANNNNCCCCAAAAAAAANTTT
TTTTNTTNTNTTTTTCTCTNGGGGNCCNNANTTNTANANTTTTNCNCCNAAAAAAA
ANGGGNCCCCTTTTTTTNCNGGNNGGNNCCCAAAANNTTTTTTTTTNAAAAAAAAAA
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35   Sequence ID 1195

GTTCGTGACNTTCGGAGCTACCTGACAGAGCAGAGTCAACCAGGNTCTGCCCAAAG
AGAGTGTTAGGCCTGAGCTTGAGAGCCCTGGAGAGACGTGTGCACAAAATGTGACC

- 247 -

TGAGGCCCTAGTCTAGCAAGAGGACATAGCACCCTCATCTGGGAATAGGGAAGGCA
CCTTGCAGAAAATATGAGCAATTTGATATTAACTAACATCTTCAATGTGCCATAGA
CCTTCCCACAAAGACTGTCCAATAATAAGAGATGCTTATCTATTTTA

5   Sequence ID - 1196   nt: 412
GTCGACGCGGCCGCGGTCGCTGGAGNCGATCAACTCTAGGCTCCAACTCGTTATGA
AAAGTGGGAAGTACGTCCTGGGGTACAAGCAGACTCTGAAGATGATCAGACAAGGC
AAAGCGAAATTGGTCATTCTCGCTAACAACTGCCCAGCTTTGAGGAAATCTGAAAT
AGAGTACTATGCTATGTTGGCTAAAACTGGTGTCCATCACTACAGTGGCAATAATA
10   TTGAACTGGGCACAGCATGCGGAAAATACTACAGAGTGTGCACACTGGCTATCATT
GATCCAGGTGACTCTGACATCATTAGAAGCATGCCAGAACAGACTGGTGAAAAGTA
AACCTTTTCACCTACAAAATTTCACCTGCAAACCTTAAACCTGCAAAATTTTCCTT
TAATAAAATTTGCTTGTTTT

15   Sequence ID 1197
CCGCCAACATGGGCCGCGTTCGCACCAAAACCGTGAAGAAGGCGGCCCGGGTCATC
ATAGAAAAGTACTACACGCGCCTGGGCAACGACTTCCACACGAACAAGCGCGTGTG
CGAGGAGATCGCCATTATCCCCAGCAAAAAGCTCCGCAACAAGATAGCAGGTTATG
TCACGCATCTGATGAAGCGAATTCAGAGAGGCCCAGTAAGAGGTATCTCCATCAAG
20   CTGCAGGAGGAGGAGAGAGAAAGGAGAGACAATTATGTTCCTGAGGTCTCAGCCTT
GGATCAGGAGATTATTGAAGTAGATCCTGACACTAAGGAAATGCTGAAGCTTTTGG
ACTTCGGCAGTCTGTCCAACCTTCAGGTCACTCAGCCTACAGTTGGGATGAATTTC
AAAACGCCTCGGGGACCTGTTTGAATTTTTTCTGTAGTGCTGTATTATTTTCAATA
AATCTGGGACAA

25

Sequence ID 1198
CAGAGGTGGGAGGATTGCTTCAGTTCAAGAGTTTGAGACCAGCCTGGGTAACATGG
CGAAACCCTGTCTTTACAAAAAATGCAAACCTTTGCCGCATGTGTTGGGGTGCGCC
TGTAGTCCCAGCTTCTCGGGAGGCTGAGGTGGGGGGACCACCTGAGCCATGGAGGT
30   TGAGGCTGCAGTGAGCCGTGATACCACCACTGTACTCTAGCCTGGGCCATAGAGTG
AGACACCCTGCCTCAGAAATA

Sequence ID - 1199   nt: 439
CCCATCCCCTCGACCGCTCGCGTCGCATTTGGCCGCCTCCCTACCGCTCCAAGCCC
35   AGCCCTCAGCCATGGCATGCCCCCTGGATCAGGCCATTGGCCTCCTCGTGGCCATC
TTCCACAAGTACTCCGGCAGGGAGGGTGACAAGCACACCCTGAGCAAGAAGGAGCT
GAAGGAGCTGATCCAGAAGGAGCTCACCATTGGCTCGAAGCTGCAGGATGCTGAAA

- 248 -

TTGCAAGGCTGATGGAAGACTTGGACCGGAACAAGGACCAGGAGGTGAACTTCCAG
GAGTATGTCACCTTCCTGGGGGCCTTGGCTTTGATCTACAATGAAGCCCTCAAGGG
CTGAAAATAAATAGGGAAGATGGAGACACCCTCTGGGGGTCCTCTCTGAGTCAAAT
CCAGTGGTGGGTAATTGTACAATAAATTTTTTTTTGGTCAAATTTAA

5

Sequence ID - 1200   nt: 526
CTGGAGACGACGTGCAGAAATGGCACCTCGAAAGGGGAAGGAAAAGAAGGAAGAAC
AGGTCATCAGCCTCGGACCTCAGGTGGCTGAAGGAGAGAATGTATTTGGTGTCTGC
CATATCTTTGCATCCTTCAATGACACTTTTGTCCATGTCACTGATCTTTCTGGCAA
GGAAACCATCTGCCGTGTGACTGGTGGGATGAAGGTAAAGGCAGACCGAGATGAAT
CCTCACCATATGCTGCTATGTTGGCTGCCCAGGATGTGGCCCAGAGGTGCAAGGAG
CTGGGTATCACCGCCCTACACATCAAACTCCGGGCCACAGGAGGAAATAGGACCAA
GACCCCTGGACCTGGGGCCCAGTCGGCCCTCANAGCCCTTGCCCGCTCGGGTATGA
AGATCGGGCGGATTGAGGATGTCACCCCCATCCCCTCTGACAGCACTCGCAGGAAG
GGGGGTCGCCGTGGTCGCCGTCTGTGAACAAGATTCCTCAAAATATTTTCTGTTAA
TAAATTGCCTTCATGTAAACTG

15

Sequence ID - 1201   nt: 613
CTTAAGTATGCCCTGACAGGAGNATGAAGTAAAGAAGATTTGCATGCAGCGGTTCA
TTAAAATCGATGGCAAGGTCCGAACTGATATAACCTACCCTGCTGGATTCATGGAT
GTCATCAGCATTGACAAGACGGGAGAGAATTTCCGTCTGATCTATGACACCAAGGG
TCGCTTTGCTGTACATCGTATTACACCTGAGGAGGCCAAGTACAAGTTGTGCAAAG
TGAGAAAGATCTTTGTGGGCACAAAAGGAATCCCTCATCTGGTGACTCATGATGCC
CGCACCATCCGCTACCCCGATCCCCTCATCAAGGTGAATGATACCATTCAGATTGA
TTTAGAGACTGGCAAGATTACTGATTTCATCAAGTTCGACACTGGTAACCTGTGTA
TGGTGACTGGAGGTGCTAACCTAGGAAGAATTGGTGTGATCACCAACAGAGAGAGG
CACCCTGGATCTTTTGACGTGGTTCACGTGAAAGATGCCAATGGCAACAGCTTTGC
CACTCGACTTTCCAACATTTTTGTTATTGGCAAGGGCAACAAACCATGGATTTCTC
TTCCCCGAGGAAAGGGTATCCGCCTCACCATTGCTGAAGAGAGAGACAAAAGA

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Sequence ID 1202
GGAATTCGCGGCCGCGTCGACCTCTGCTCGAATTGACAGAAAAGGATTCTGTGAAG
AGTGATGAGATTTCCATCCATGCTGACTTTGAGAATACATGTTCCCGAATTGTGGT
CCCCAAAGCTGCCATTGTGGCCCGCCACACTTACCTTGCCAATGGCCAGACCAAGG
TGCTGACTCAGAAGTTGTCATCAGTCAGAGGCAATCATATTATCTCAGGGACATGC
GCATCATGGCGTGGCAAGAGCCTTCGGGTTCAGAAGATCAGGCCTTCTATCCTGGG
CTGCAACATCCTTCGAGTTGAATATTCCTTACTGATCTATGTTAGCGTTCCTGGAT

CCAAGAAGGTCATCCTTGACCTGCCCCTGGTAATTGGCAGCAGATCAGGTCTAAGC
AGCAGAACATCCAGCATGGCCAGCCGAACCAGCTCTGAGATGAGTTGGGTAGATCT
GAACATCCCTGATACCCCAGAAGCTCCTCCCTGCTATATGGATGTCATTCCTGAAG
ATCACCGATTGGAGAGCCCAACCACTCCTCTGCTAGATGACATGGATGGCTCTCAA
GACAGCCCTATCTTTATGTATGCCCCTGAGTTCAAGTTCATGCCACCACCGACTTA
TACTGAGGTGGATCCCTGCATCCTCAACAACAATGTGCAGTGAGCAT

Sequence ID - 1203   nt: 692
TGCAGAGGGGTCCATACGGCGTTGTTCTGGATTCCCGTCGTAACTTAAAGGGAAAC
TTTCACAATGTCCGGAGCCCTTGATGTCCTGCAAATGAAGGAGGAGGATGTCCTTA
AGTTCCTTGCAGCAGGAACCCACTTAGGTGGCACCAATCTTGACTTCCAGATGGAA
CAGTACATCTATAAAAGGAAAAGTGATGGCATCTATATCATAAATCTCAAGAGGAC
CTGGGAGAAGCTTCTGCTGGCAGCTCGTGCAATTGTTGCCATTGAAAACCCTGCTG
ATGTCAGTGTTATATCCTCCAGGAATACTGGCCAGAGGGCTGTGCTGAAGTTTGCT
GCTGCCACTGGAGCCACTCCAATTGCTGGCCGCTTCACTCCTGGAACCTTCACTAA
CCAGATCCAGGCAGCCTTCCGGGAGCCACGGCTTCTTGTGGTTACTGACCCCAGGG
CTGACCACCAGCCTCTCACGGAGGCATCTTATGTTAACCTACCTACCATTGCGCTG
TGTAACACAGATTCTCCTCTGCGCTATGTGGACATTGCCATCCCATGCAACAACAA
GGGAGCTCACTCAGTGGGTTTAATGTGGTGGATGCTGGCTCGGGAAGTTCTGCGCA
TGCGTGGCACCATTTCCCGTGAACACCCATGGGAGGTCATGCCTGATCTGTACTTC
TACAGAGATCCTGAAGAGAT

Sequence ID 1204
TTTTTTTTTTTTTTCCTGCGGGAAAGCGCGCCATTGTGTTGGTACCCGGGAAATTCG
CGGCCGCGTCGACACAGGCCCCAGCATCAAGATCTGGGATTTAGAGAGGAAAGATC
ATTGTAGATGAACTGAAGCAAGAAGTTATCAGTACCAGCAGCAAGGCAGAACCACC
CCAGTGCACCTCCCTGGCCTGGTCTGCTGATGACACAGGTTGGGCNGGNNCNCNGG
GGNGGNNNNGNNNNGCNGNNGGNNCNGNNNNCNNNNNNGCNNNNGNNNNTNNNCNNN
GNNCNNNNNNNNNNNNNNNNNNNGNTCNNGNNGCNGGGGCCNGGNCGNCGCGGNCGCG
NNTNNNNGGGTNCNNNCNCNNNGGCGCGC

Sequence ID 1205
CAGACTCTGACCCAGCCTCAGTCCTAACTCCTGGGGCTGGGCTGAGGGGAACAAGC
ATTTGCTGAAACTTGAAAAAACAAAGCAAATCAAAAACAGGAAAAAATTGTACCTG
GTACTTTTTTTTAGAAAAAAAGATTAAAAAAGAAAGAATAAATTCTTGTTTGGAAA
CTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAATTTTAAACTC

- 250 -

TNNNNNTNNCNNCNANTAANNCANNTCNANNNNANNNAATTACTTNNANGTNNNTC
ACN

Sequence ID - 1207   nt: 642

ACGAGAAGCCAGATACTAAAGAGAAGAANCCCGAAGCCAAGAAGGTTGATGCTGGT
GGCAAGGTGAAAAAGGGTAACCTCAAAGCTAAAAAGCCCAAGAAGGGGAAGCCCCA
TTGCAGCCGCAACCCTGTCCTTGTCAGAGGAATTGGCAGGTATTCCCGATCTGCCA
TGTATTCCANAAAGGCCATGTACAAGAGGAAGTACTCAGCCGCTAAATCCAAGGTT
GAAAAGAAAAGAAGGAGAAGGTTCTCGCAACTGTTACAAAACCAGTTGGTGGTGA
CAAGAACGGCGGTACCCGGGTGGTTAAACTTCGCAAAATGCCTAGATATTATCCTA
CTGAAGATGTGCCTCGAAAGCTGTTGAGCCACGGCAAAAAACCCTTCAGTCAGCAC
GTGAGAAAACTGCGAGCCAGCATTACCCCCGGGACCATTCTGATCATCCTCACTGG
ACGCCACAGGGGCAAGAGGGTGGTTTTCCTGAAGCAGCTGGCTAGTGGCTTATTAC
TTGTGACTGGACCTCTGGTCCTCAATCGAGTTCCTCTACGAAGAACACACCAGAAA
TTTGTCATTGCCACTTCAACCAAAATCGATATCAGCAATGTAAAAATCCCAAAACA
TCTTACTGATGCTTACTTCAAAAAGA

Sequence ID 1208

CCCTATACCTTCTGCATAATGAATTANCTAGAAATAACTTTGCAAGGGAGAGCCAA
AGCTAAGACCCCCGAAACCAGACGAGCTACCTAAGAACAGCTAAAAGAGCACACCC
GTCTATGTAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAG
CCTGGTGATAGCTGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTTGCCCA
CAGAACCCTCTAAATCCCCTTGTAAATTTAACTGTTAGTCCAAAGAGGAACAGCTC
TTTGGACACTAGGAAAAAACCTTGTAGAGAGTAAAAAATTTAACACCCATAGTA
GGCCTAAAAGCAGCCACCAATTAAGAAAGCGTTCAAGCTCAACACCCACTACCTAA
AAAATCCCAAACATATAACTGAACTCCTCACACCCAATTGGACCAATCTATCACCC
TATAGAAGAACTAATGTTAGTATAAGTAACATGAAAACATTCTCCTCCGCATAAG

Sequence ID - 1209   nt: 620

CTCTCCTGTCAACAGCGGCCAGCCTCCCAACTACGAGAATGCTCAAGGAGGAGCAG
GAAGTGGCTATGCTGGGGGCGCCCCACAACCCTGCTCCCCGACGTCCACCGTGAT
CCACATCCGCAGCGAGACCTCCGTGCCCGACCATGTCGTCTGGTCCCTGTTCAACA
CCCTCTTCATGAACACCTGCTGCCTGGGCTTCATAGCATTCGCCTACTCCGTGAAG
TCTAGGGACAGGAAGATGGTTGGCGACGTGACCGGGGCCCAGGCCTATGCCTCCAC
CGCCAAGTGCCTGAACATCTGGGCCCTGATTTTGGGCATCTTCATGACCATTCTGC
TCGTCATCATCCCAGTGTTGGTCGTCCAGGCCCAGCGATAGATCAGGAGGCATCAT
TGAGGCCAGGAGCTCTGCCCGTGACCTGTATCCCACGTACTCTATCTTCCATTCCT

- 251 -

CGCCCTGCCCCCAGAGGCCAGGAGCTCTGCCCTTGACCTGTATTCCACTTACTCCA
CCTTCCATTCCTCGCCCTGTCCCCACAGCCGAGTCCTGCATCAGCCCTTTATCCTC
ACACGCTTTTCTACAATGGCATTCAATAAAGTGTATATGTTTCTGGTGCTGCTGTG
ACTT

Sequence ID 1210
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GGGCCGGAAGGGACTATTTAGATCATCCAGTCCCACCCTGTCATTTATGGAGGAG
GAAACTGAGGCCTAGATAAGATAACCAGTTAGTGGGTCCACTGACCTTTAGGACAG
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CCTTTAGTCTTATTTGAGCTCATCTGTGCTTTTAATGTGTACTACGTTAGGTGTTT
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Sequence ID 1211
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TAGAAATGAATGGAAGATGATGGGAAATATGACTTCACCAAGGAGCAATGCTGGGA
TTGCAACTGTAGGGAACACCATTTATGCAGTGGGAGGATTCGATGGCAATGAATTT
CTGAATACGGTGGAAGTCTATAACCTTGAGTCAAATGAATGGAGCCCCTATACAAA
GATTTTCCAGTTTTAACAAATTTAAGACCCTCTCAAACTAACAGGCTTAGTGATGT
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ACTTTTTGGGTTTATTTGGAAAGGAATGCAAAGATGAAGGTCTGTTTTGTGTACTT
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Sequence ID - 1212   nt: 374
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CAAAGTGACCAAGAACGTGAGCAAGCCCAGGCACAGCCGACGCCGCGGGCGTCTGA
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TACGAGCGGCGCGCCATGGAGTTACTGAAGGTCTCCAAGGACAAACGGGCCCTCAA
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CCCCTGCCCTCTCCCTGAAATAAAGAACAGCTTGACAG

Sequence ID - 1213   nt: 567
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GCCTACAGTTCCACCACTGTGACCTCTGAAAACCTCCTGAACAAAAGGAAGGAGAC
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TGTGAGTAAATGACATCTGTCACCTGTGACACGGGCCAGGGACTATCACCATATGG
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ACCAGCC

Sequence ID - 1214   nt: 620
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CCACATCCGCAGCGAGACCTCCGTGCCCGACCATGTCGTCTGGTCCCTGTTCAACA
CCCTCTTCATGAACACCTGCTGCCTGGGCTTCATAGCATTCGCCTACTCCGTGAAG
TCTAGGGACAGGAAGATGGTTGGCGACGTGACCGGGGCCCAGGCCTATGCCTCCAC
CGCCAAGTGCCTGAACATCTGGGCCCTGATTTTGGGCATCTTCATGACCATTCTGC
TCGTCATCATCCCAGTGTTGGTCGTCCAGGCCCAGCGATAGATCAGGAGGCATCAT
TGAGGCCAGGAGCTCTGCCCGTGACCTGTATCCCACGTACTCTATCTTCCATTCCT
CGCCCTGCCCCCAGAGGCCAGGAGCTCTGCCCTTGACCTGTATTCCACTTACTCCA
CCTTCCATTCCTCGCCCTGTCCCCACAGCCGAGTCCTGCATCAGCCCTTTATCCTC
ACACGCTTTTCTACAATGGCATTCAATAAAGTGTATATGTTTCTGGTGCTGCTGTG
ACTT

Sequence ID 1215
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AGTCCAAGTAAATGATCACTTTATTTGCTAGGGAGGGAAGTCCTAGGGTGGTTTCA
GTTTCTCCCAGACATACCTAAATTTTTACATCAATCCTTTTAAAGAAAATCTGTAT
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5 AAACATGGTAGTACTGGAAATTTTACAAGACTTTTACCTAGCACTTAAATATGTAT
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CTCTCTGTACATTTGCTAGCTTGTAGTTTTCTAAGACTGAGTAAACTTCTTATTTT
10 TAGAAAGTGGAGGTCTGGTTTGTAACTTTCCTTGTACTTAATTGGGTAAAAGT

Sequence ID - 1216   nt: 484
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15 ATAGCAAGGACTAACCCCTATACCTTCTGCATAATGAATTAACTAGAAATAACTTT
GCAAGGAGAGCCAAAGCTAAGACCCCCGAAACCAGACGAGCTACCTAAGAACAGCT
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20 AAGAGGAACAGCTCTTTGGACACTAGGAAAAAACCTTGTAGAGAGTAAAAAATT
TAACACCCATAGTAGGCCTAAAAGCAGCCACCAATT

Sequence ID 1217
GACAGGCGGGGGCCCAGCGGCCGGGTGAAGGCCGGGTGGCTCTGTGAATCAAAGGA
25 GAGTCCCAGAAAACCTGTGACTGTTGAAGAAAATTCATCTGTGAATTTTTATATTC
AAGGAGTCAGTATTTATATTCATCTTTTAAACTGGGAAGATTTATATTTTACTTTA
AAACTTCTTGATAATAATTTACAATGAATGGACACAGTGATGAAGAAAGTGTTAGA
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30 TCATAGGTAGCAGAGTTTTCAGGTTTTCCTCTTAGCTATCCAAATACTAAAAAAAT
TCTGATATACGAACCTTTTTTCATAATACAGGTTTTAATTATATTTTTCATTCAGA
TACACAGTAGATCTTAAATATAGAAAGTTTTTGTTTACTTAAATCTATTTGGAAGT
TTATATTTGAGCTAATAATTAAGCTGGAGCATGTATAATAGATTTAAATTGTTTTG
ACTGTTAGTGAAATTT

35

Sequence ID 1218
CTCACTTGGTGGGTGAGCCTCCAATGACTACACCCAAGGAGGATTTAACACAGGGA

- 254 -

TTTTATGACTTGCAACAAGTCAGGAGGACATGGGGTTGGGGTAGTTCAGCAGTGCC
TGTCTGAACAAAGGTGAAAATTGGGCTTTTATTGGGCTGATCAAGGGGGAGTAAAG
GCAGCCAGGAGCAGTCGCCTGTCATGCTTCTACCTATATTGCATGTATAGAAAAGG
GAAAATAAACTCCTTCCTGGGCAGGGTTTTAGTATGCTAAGGAGGGGAGTTATTCA
5   ACTTCAATCCAACTCAAGCATCAGCATTGCTGCGTCCATCCCAGTTTTGTTTTGCT
GGGGCTGAACTTCTTCCTATAACTTTTTGAAACAACAAGAACTCAAGGTGTGACAG
TTACAAGTGGGCCCTTTTTCACAGTGTGTACCTAAACACGTGAGGACCCTGGATTA
CAGAATGACAGACTCGAAGTGACTCAAGTTCCGGTTGTTCATCTTTAGATGGTAAA
GATGGCTGTACGTACTATCCTTGCTTATTTCCAATCTATTGTTTAAACTCTTGTAT
10   ATGTAATACCGCAGAGGCTAGAGATACAACCTTTGACCAAATGAGTGAATTCAAGT
AATCCATTACTAATGTGATCTGGAAACAAACATGGTGTTGAATGTGCATATGT

Sequence ID - 1219   nt: 559
CTTGGCAGCTCCGTTATGTGCCCAGCTCTTTGCAAGGGCATACTGGGAAATGAGTG
15   GAGATAAAGGACCCAATCATAAGCATTTTACAGTATGGATACCCCATTTTAAAAAG
GTAAACTGAGGCACAATGCAATTTTTTTTTTTTTTTAAGGAGTTTATTTGAGCAAA
CAGTGATTCATGAATCAGGCAGCACCAAACCAGAAGGAGGCTTTGCTGAANAAGGA
TGAGGGACAAGCATTTATAAAGTGAATGTAGATGTAATACAAAGAAAATATTTGAA
CCGGGTGCGGTGGCTTACACTTGTAATCCCAACACTTTGGGAGGCCAAGGCGGGCA
20   GATCACAAGATCAAGAGATCGAGACCATCCTGGTCAACATGGTGAAACCCCATCTN
TACTAAAAATACAAAAATTANCTGGGCGTGGTGGTGCGTGCCTGTAGTCCCAGCT
ACTTGGGCGGCTGAGGCAGGANAATTGCTTGAACCCGGGAGGTGGAGGTTGCAGTA
AGCCGAGATTGCACCATTGCACTACTCCAGCCTGGTGACAGAGAGAGACTCCATC

25   Sequence ID 1220
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CCCCCNNANNTNNCATAAGAGAGATNACTACNGTACANATAGNGNCANACNGATA
GTAGTANCAANATTGTNTTAGCTANATNANTCAATAGATATCNAGATANAANAANA
NCNNGGATATACAGCGATGTNTNANNGGNNNNNNNANGGAACGAACATCNACNTTA
30   ANNATAAGCTNGNGGAGAGAGACANGTANGTTATANANNAGAATNGNAGTAGGNGT
GATCATAATAGNNNNNNANNTANTATATANGATNTTANTGNNCTNTNNTNNGTTTAT
CNNNAATNTCTATNCTNGAGAGNAGCNNNATNNNNAGGCGANGANATTGGGNNNTN
CTCNTNATAGANANCTGGTGTCNNANAANTACNTCATCTATTNANCTCTCACNANA
TGGNANNATANAGNAGNGNNNTNNANAGGANTANGCATAGNGNNTNNCTNAAACAA
35   AANNNATAAGANNTCTCGNNAANANGGGCCTNTNNTNTAGCGAGGNNTTANTTTNT
ATANTTNTTCNCTCTTNNAATANNTANGATANATGANCTNGNNGTGATANATANNN
NNTACNGTNAANNTNTANTCNTATAATAGATANAAATATAGGATNTTNCTCTGGCN

- 255 -

GGTNGAANANTTNNTNCNNTTTNAATAATGNTGTTAGNGACNGNGNTNTNANANNN
NNTTAGAAAGGTACTCTATATACTNNTATGNTNCGGCNNATAATANAACAGATGTT
TGTATNAATATNAAANAAGGTCNNTTTCGNCAAGAGAANNNTGNCTGGTNATAGAA
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NAGTCATTNNGNATNTATNNNGNNTANTAGTNANTTGGGNCTNNTNCAGANTATAT
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TATTAANCNANNATCACANTATANCNGNGACANNNGCGANANTATATGTATGNNAN
TATNACNGNTCCNNNCCGNGAANNTANTCNTANNAGGCATTCNGNNGAGCTNTTCT
NCTAGACNATTTNNANTGAAANNATGCNGNNAAAAACGACNNNCTTNAANTTNTGT
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NGCTNNNACT

Sequence ID - 1221   nt: 741
         AAGCAGAANTNTCTCTAAAAACATTATCTCCTTAAAATCTTGAGGTGCATATNAGA
         GCCACAGGCAATCTCTGACATATAAAATTGCAGTACAGGCCTTTCAAATTTGGCAT
         TTCACTGGTACAATACAACAACCAAGATATATAATAACTGTACAGTGCCTAGACAT
         TCCAGTAAGAACCATTATTTTCTTTAATGTAGAATGATTAATACATATTCTACAAG
20   GGGCAGTAAGGTTAGTAATTCTATAGGGTATGTCCCGACATAATTTTCAAATTGTA
         CAATAACACAAACAACTTTGTTAAGGCCATGTTTTATTTGCTGATTAATGGACAAA
         AGGCAATGTAATTTATTTTCAAGTATTTTCTTGAAAGTCTGTGCTCATAAAAATCA
         TGAAAGTTGGAAAGACTGTTAAATCACTGAAACTTCAAATATATCTTACACAATC
         TTGTTTGTACAAAAATACAAGTTAAATATAAACATAAAGCAATCATGGTAATTTTA
25   TGCAAATCTGTTTTATGTGATCATCAGTTATATATAAAAGTTTCTCAGTTCTGTTA
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         AAGCTTACTTTAGCACTCATCTTTTACATGGTTAAATGCATTTCCTAATTTGAGAT
         CACCTAAACACTGGAAAAGAAAAAAAATGAAAGGGCAGTATGTCCATAAACCAACA
         AATAATTTGGCTG

30

         Sequence ID - 1224   nt: 485
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         GGGAGTATTTCAGGGTTCACTTCAGGGGCTCCCAAAGCGACAAGATCGTTAGGGAG
         AGAGGCCCAGGGTGGGGACTGGGAATTTAAGGAGAGCTGGGAACGGATCCCTTAGG
35   TTCAGGAAGCTTCTGTGCAAGCTGCGAGGATGGCTTGGGCCGAAGGGTTGCTCTGC
         CCGCCGCGCTAGCTGTGAGCTGAGCAAAGCCCTGGGCTCACAGCACCCCAAAAGCC
         TGTGGCTTCAGTCCTGCGTCTGCACCACACAATCAAAAGGATCGTTTTGTTTTGTT

TTTAAAGAAAGGTGAGATTGGCTTGGTTCTTCATGAGCACATTTGATATAGCTCTT
TTTCTGTTTTTCCTTGCTCATTTCGTTTTGGGGAAGAAATCTGTACTGTATTGGGA
TTGTAAAGAACATCTCTGCACTCAGACAGTTTACAGA

Sequence ID 1226

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CACTTGGACAGCAGAGGGGGTGACTCTGCCCATCCCTGCCACTGGTAGCCAGGCGG
GCAATGTCTGCTAGCAGTCTGCTTCTGTCTGAACTCAGCCAGCAGAGGCAAACTCC
CGGTTCCCCGAGAAACACTCTGAAGGCAGGGTGGGTGACTCCACCCACCACCGCCT
CTCCTAGCCATGCAGGCCATGTCTGCTAGAGCTTCCAGCGCAGTGGTCCTAATTCT
GTCTGAATCCGGCTGAGGGGTGCAGCCTCCTGTTACTGCCCAGGGAAACACCCAGA
TGGCAGGGTGGGTGACTCCAACCACCTCTGCCTGTGGTAGCCAGATGGGCCACACC
TGCTAGAGCTTCCAGCCCAGCAGTCCCGCTACTCTGTGGGTGGGTGCCATCCCCTG
TTCCTCTGGGAAGCACCCAGACAGCTGATTACGTGACCCCACCCACTTCTGCAGAT
CCTAGCTGAGCAGGACTTGCTGGTTTGGACAATGCCCAAGCAGGGAAGAGCCCTCA
TTCTCTTATCACTGACAGAGGTGAGATGTCCGANTTTGTANGCTGGTGGAGGAGTG
AGGTGGAGGAGGTATGCCTCT

Sequence ID 1228

GTTATTCAGGTATCCATCAAAATTTTATAAGAGGGCCGGAAACATCGGCTCACACC
TGTAATCCCAGCACTTTGGGAGGCTGAGGCAGGTGGTTCACTTGAGGTCAGGAGTT
CGAGACCAGCCTGGCCAACATGGCAAAACCCCGTCACTATTAAAAATACAAAACAT
TAGCTGGGTGTAGTGGCAGGTGCCTGTAATCCCAGCTATTCGGGAGGCCTAGGAAG
GAAAATGGCTTGAACCTGGGGGTGGAGGTTGGAGTGAGGCAAGATCACACCACTGC
ACTCCAGCCTGGGCGACAGAGCGAGACTCCATCTCAAAAGAAGAAAAAAAAAACAA
CAAAAAAACCTTTATCAGATTATCAGAGGTTATCACTACAGAGGGAGGTAAAATTG
GAGGGAAAAGGGTACAAATTTATTTCAC

Sequence ID - 1230   nt: 741

AAGCAGAANTNTCTCTAAAAACATTATCTCCTTAAAATCTTGAGGTGCATATNAGA
GCCACAGGCAATCTCTGACATATAAAATTGCAGTACAGGCCTTTCAAATTTGGCAT
TTCACTGGTACAATACAACAACCAAGATATATAATAACTGTACAGTGCCTAGACAT
TCCAGTAAGAACCATTATTTTCTTTAATGTAGAATGATTAATACATATTCTACAAG
GGGCAGTAAGGTTAGTAATTCTATAGGGTATGTCCCGACATAATTTTCAAATTGTA
CAATAACACAAACAACTTTGTTAAGGCCATGTTTTATTTGCTGATTAATGGACAAA
AGGCAATGTAATTTATTTTCAAGTATTTTCTTGAAAGTCTGTGCTCATAAAAATCA
TGAAAAGTTGGAAAGACTGTTAAATCACTGAAACTTCAAATATATCTTACACAATC

- 257 -

TTGTTTGTACAAAAATACAAGTTAAATATAAACATAAAGCAATCATGGTAATTTTA
TGCAAATCTGTTTTATGTGATCATCAGTTATATATAAAAGTTTCTCAGTTCTGTTA
TTTGTGAAAAGATCAATACCAGATTGAATGACTACCTATTGGCAAAGGGCCCTAAA
AAGCTTACTTTAGCACTCATCTTTTACATGGTTAAATGCATTTCCTAATTTGAGAT
CACCTAAACACTGGAAAAGAAAAAAAATGAAAGGGCAGTATGTCCATAAACCAACA
AATAATTTGGCTG

Sequence ID - 1231   nt: 203
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ACAGTCCCTTAACCTGCCACGGGAGAGGGGCCCCCAAACTTTCTTCCCCCCACACT
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AGGAGAGATGCTGGAGGTGGGGGTGCTGTGTTCTA

Sequence ID 1239
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TACAAAAATATAGCAATACAGNGAACTTCACCAAATCCTAAATATTCAGTACCTGA
ACTGGCTACAACACCGNGTGCACACCCAGTTCCTGCAGAATCTCTTGCAGATATGG
GAGAGTCAGCCAGTGAAAAGATCCATTTCTTGGGAATCCTTGTCAACAAGACCAGT
TCAGAAATCCAGGATATATAGAAGCCTACTGTAATTTAAAAACAGTAACAAAAACC
CCAACAAAACCCAAATCAACAAAGACCAAGATAAAGGNGTGATAAACATTAATTGT
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AANGGGCAAAAAAAAAAATCTAGACTCGAGCAAGCTTATGCATGCATGCGGCCGCA
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TCGNCTTGNAACAATNCCCNTTTNGCCAGNGGGG

Sequence ID 1255
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GGGCCGGAAGGGACTATTTAGATCATCCAGTCCCACCCTGTCATTTTATGGAGGAG
GAAACTGAGGCCTAGATAAGATAACCAGTTAGTGGGTCCACTGACCTTTAGGACAG

- 258 -

TAGTCTATCCGTAAGAGACAACATGGAGAAAGAAATACAACGTTTTTATAGTGAAT
TATCATCTTACAAAGAATATTCTTCCCATATCGCACTTTTAAAAAGTGGGTACCTT
AGTCAAATAGGAGAAAAAACCACTTGAGTAGTTTCATCCTCAGGTTTTAGGTGAGG
AAACTGATACTCAGATTAAATAACTTTAAGCACACAGAGCCTGAATGATAGTCTTA
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CCTTTAGTCTTATTTGAGCTCATCTGTGCTTTTAATGTGTACTACGTTAGGTGTTT
TCACTTGCATTTCCTTGTTTGACGTTGACAATAAATCGTGAAGCTGCCTTATCTAA
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CAGGTNTCAAATATAACTGAAAACCCATGCTAACTGACTNATTTTAAAAGNTGTNT
GGGGCATGAAANGATTGCTCTGCCTGGGCGGGNGGTTNANCCTGNGTCCCCCNTTT
NGGAGNCCACCCANGANGCGATATTTNAGGGNNGATTCNAAACCCCTGGCACGNGN
NAACCCCNTTTTTAAANANAAAANANCGGNNG

Sequence 1256

TTGTGTTGGTACCCGGGAATTCGCGGCCGCGTCGACGGAGTTTTACCTTATTACAC
TTTAATCTCTGGATTTACCCCATCTCATTTCTCTTTTAGGAAAACTGTTTGTATGT
GGTGGCTTTGATGGTTCTCATGCCATCAGTTGTGTGGAAATGTATGATCCAACTAG
AAATGAATGGAAGATGATGGGAAATATGACTTCACCAAGGAGCAATGCTGGGATTG
CAACTGTAGGGAACACCATTTATGCAGTGGGAGGATTCGATGGCAATGAATTTCTG
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AGACTTTGGTTATTTTACTTTTTGGAAAAGAATAAACCAAGAATTGATTGGGCACA
TCATTTCAAGAAGTCCCCTCTCCTCCACATTTGTTTTGCCAATTTGCACATTAAAT
GACTCTTCCCTCAAATGTGTACTATGGGGTAAAAGGGGTAGGGNTTAAANATGTAA
ACAGTTGGGTTTTTTAAGGGNCCTTTTTCATAACTGGAACACTCTNTACAAGGNTN
CTTNTTAAATAAATAACTTGACTTTTTTGTTTTNTAAANGNANCTTCNTGCTTCCA
TAAAAAAAAAATTTAANTNGNCANCTNTGCTGCTGCGNCCANTTNGCTNGNCCNT
GGCATTCCCTAGGGANGNTNAATANTGGCNNNTTAACNNGGCNGNAACNNNNNCCA
NT

Sequence ID 1331

GGGCGATGCATGCTTTATTAAGGCTCTTGTTTCACCTGGCAGTGTACTGTATCAAC
GTATAATACAGAAAAAAAATCTCTTTAAGGTCCTCCTTCACAAAGACATAGAGTGA
AACTCCCTTTACATGTCAGTATTTGTTCAACACTTTAGGCAACTTGACTGTCAGTG

- 259 -

TTAAAATGGAAAACAGGAAAATGGAAAAATCTGACCAATTCTGCCACCTTGAGACT
TTCATATAGACCTTGCACAACAATTGTATAGATCACACACCGGCTGTATTTAATAT
GTAACATTTTCACACATATTAAAGATACAGAAGTATTAAAAAACCCCCAATGTTAA
TGTATTTGCTTAAAAGGCACAAGTTTCACATATCTGTCTAGCTATCTGTTGGTAAT
5   ACAGAAAGTATACTACTTTTTTAAAAAAGTGGGCAGAATTCTTGTGTATGTATATT
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GTGAAGAAATATTTCAAAATGGCCATAAAGGAGGTAAAAATGAAAACCATAACCTA
ACTTTTATAGAGGCTTTATCTTTAATTTAACGATGTGCGGAGGACTTTCTTGCTTG
10   AATCTGTTCCGGCTGTCTGCTCTGTCCATCAAATGGGCAGGTCTGGGAATGAGGC
ACCTTCGGCCGTTCAGAAGTGGCCTGAACAGAATGCTGGAACCCAGGCTGGACTCG
GAC

        Sequence ID 1332
15   CAAACCTGCATGTTCTGCACATGTATCCAGGAACTTAAAAAAAAAAAAAGATAGTT
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20   AATATGGATTAAACATCTGTGGGTTTTTAATATGGGTTAAAAATCAAAGAAAATG
AACTATTTGCTCCAGTGCAGGAAAATACAGGCAATACTGGATACAATTAGATGGTC
AGGAGCGATAACCCGGTTGCCATTGTTTGAAGAAGAGAATAAGGTGCTAGCATTCC
TATCCGTAGATAATTTGACAGCTAGGAAATAGGGGGAGTCTTCTATGTAGTTAGTG
AAGGCTAAATGAACTATTATATGCAGTTATCGTAGAAGAGTACTCAAAAAAATCTG
25   TAAAAAATAAAGAAAGGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTG
GGAGGCCGAGGCGGGTGGATCATGAGGTCAGGAGATCGAGACCATCCTGGCTACCA
NGGTGAAACCCCCGTCT

        Sequence ID 1335
30   CAAGACTCCATCTCAAAAAAAAAAAAAAATCTACAGTGCTGAGTATATAAAATTAT
TAACACATTTCACAACAATATGTGTTTGTGGAGTTAAATATTTTTTGTCTTTAAAA
CAGGTAATTTTAGTGCATACTTAATTTGATGATTAAATATGGTAGAATTAAGCATT
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35   ACAATTACTGGTGTTTAACTGCCAAATATGGGTAAATAAGGGAAAATTTTGTTTAA
TATTTAGTCCTTCTGAGATGGCTTGAATATTTGAATTTTGTTGTACGTCTATACTG
GGTAGTCACAAGTCTTATAAACACTTTAGAGGAAAGATGGATTTCAGTCTGTATTT

- 260 -

TTAAACATCATTTATTTTAAATCTGGTGCTGAAAAATAAGAAAAAAATTAAACTGC
ATTCTGCTGTTCTTCTTTAGAAGCATTCCTGCGTAAATACTGCTGTAATACTGTCA
TGCAAAGTGTATCCTTTCTTGTCGTATCCTTTTTGGGGCAGTGTTTTTTTGTTTTT
TTCCTAGAAATGTTTGTCCTTCCCCCACCTGTTGATCCAGGTTAAGGAATACTTTT
5   TTACACTTTATTCAAA

Sequence ID 1336
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TGTGAGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCTC
10   GACATTCGGGAAGTGTTTTTGAGAAGTCTCGGTCGGTAAGGGAAGTCTTCCAAGTC
CGTGCAGCACTAACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCCAGATGAGG
CAGCTGTGACTGTGTCAAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTT
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Sequence ID 1337
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25   AAACCACAGATGCAGGAAGCTTAAACACCAACAGGATAAATAAAACAAAATCTACG
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GACTTCCCTTCAGAAATCTTGCAAACAAAAGATGTAGCACAATATTTAAAGTATT
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30   GGCAGGAGGACCATGAGGTCAGGAGATCGAGACCATCCTGGTGATGGTGATACCCC
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Sequence ID 1338
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5 ATTAGTTGACTGGTGTTCATATGCAAGGCAGTCTACTGGGTGCAACAAGGGTTAGA
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10 ACATTGGGCACTTATTCATTCTCTGAGTAAATATTTATTGCATGCTTATCTTGTAT
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15

Sequence ID 1344
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20 AGTAAAGTTGATATCTTCTGGATGTATACTAATTTTAGGCTTTATTTTAAAACTGC
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25 AAACCCCATCTCTACTAAAAATACAAAAATTAGCTGGGCGTGGTGGCACACGCCTG
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30 Sequence ID 1348
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Sequence ID 1351

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TCTCTCCATTTGTAGAATGTGAAATTCTTTAAAATGCATCCTATATTAGGAATACT
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TCAGCACAGCGTGACTGCCTATCAGTGACAATATAAGTGAGCTCTATTTGGATCCC
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Sequence ID 1352

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TAAAATCACTGGCATGTTGTTGGAGATTGATAATTCAGAACTTCTTCATATGCTCG
AGTCTCCAGAGTCACTCCGTTCTAAGGTTGATGAAGCTGTAGCTGTACTACAAGCC
CACCAAGCTAAAGAGGCTGCCCAGAAAGCAGTTAACAGTGCCACCGGTGTTCCAAC

- 263 -

TGTTTAAAATTGATCAGGGACCATGAAAAGAAACTTGTGCTTCACCGAAGAAAAAT
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Sequence ID 1353
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Sequence ID 1355
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Sequence ID 1359
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CAATGGAGTGTGCATTACATTTGGAAAAAATGTGAATCAGTCACTACTGGAACTGC
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- 264 -

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TACC

Sequence ID 1360

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Sequence ID 1361

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ACTG

Sequence ID 1364

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Sequence ID 1365

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Sequence ID 1366

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Sequence ID 1367

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Sequence ID 1368
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25 GACACCTGTGATAGGACAATAAAAT

Sequence ID 1369
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30 ATAATGTAAATAATACTTAAGAAAATAAGATCTCAGGAAACTGTGTATACTCTGTA
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35 Sequence ID 1370
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Sequence ID 1371
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Sequence ID 1372
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Sequence ID 1374

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Sequence ID 1378

CTGAGTATTAACTAAAAAAAAAAAAAAAAAAAAAAAAAAA

Sequence ID 1380

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Sequence ID 1382

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Sequence ID 1387
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Sequence ID 1389
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Sequence ID 1390
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ATGGTTGGAAGACCTAGATCTGGGCCCAATGGCCAGACACCCTGCTTGACCTTGGC
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CTTAGGAGAGGAGT

Sequence ID 1391
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CTAGGAGCTATGGTGGCTGTTGTGATGTGTAGGAGGAAGAGCTCAGGTGGAAAAGG
AGGGAGCTGCTGTCAGGCTGCGTCCAGCAACAGTGCCCAGGGCTCTGATGAGTCTC
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Sequence ID 1392
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AAAACTACAAATTTTTATTAAATTAATAAATCAGAATACTAAATCCATGTGTTTTT
TTCTTTCTTAAAAAATATCTTTTGGCTGGGCACGGTAGCTCATGGCTGTAATCCCA
GCACTTTGGGAGGCTGAGGTGGGTGGATCGCCTGATGTCAGGAGTTCAAGACCAGC
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Sequence ID 1394
GCATAATGTGAGGAGGTGGAGAGACAGCCCACCCCCGTGTCCACCGTGACCCCTGT
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TTCCCTACTGAAAATAAGAATCTGAATATAAATTTGTTTTCTCAAATATTTGCTAT
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Sequence ID 1395

CTTACCATGTCAGTGCACAGAAATGCTGTCTTGGGATGTAGGAAAAATAAATCCAC
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AATATCAGCCTGTCTCCTAGGTCAGTCCCCTCCTGGACCCACCCGCTCCCTTTTTT
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CTGGACAGAACTGAAACACAGCAACACCAGTTCTCAAGGACAAGGTGTGTGATGGG
GGTAGGAAGCTTGGTGCTTATGTAACCATTTTAAACGTGGTTTCTATAGGAAAGAC
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Sequence ID 1396

CAAACACTATGTTATTTTATGAANAAGACTTGAACATCTATGGATTTTGGTATTTG
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TGTAAACTGTATAAGTAATGAAATTAAAAGGCAGAAATTGTCAGACTGAATAAAAT
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CACCACCAACAGCAGAGTACATATTATTTTCAAGTACACAGAAAACAGTTACCAAT
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TATATAAAGTATGTGCTCTGACCNCAAAGGAATTAGAGATCAATAAAAGAACATCT
TTGAAAAATCTCACNTATTTAAAAACTAATAACTCACTTCTAAATAACTCCTGTNT
CAAGAGAATNAAANGG

Sequence ID 1397

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GGGGGTCAAGGGCCATGGGGGCAGGTAGCTCTGCCTGCAAAGCCCACAAGCATGTC

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TCCTGGCCTCGCTGAGCAAGTGCAGAAATTTTTACCTTCAAGGATCAGGGTTTTTC
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GCAGAAGAAGCGTCTGGTAAGACAACCAGCAAGTTAACAATGGTCACCTCCAGAAA
5 TGGGCTGGGTAAACCAAAGAATTTTTTTGTTTTTGTTTTTTTTTGAGTCAGGGTCTA
GCTCTGTCACCCAGGCTGGAACGCACTGGTGTGATCACGGCTCACTGCAGCCTTGA
CCTCCCTGGCTCAAGCAATCCTCCCAGCTCAGCCTCCTGAGTCGTTGGGACTACAG
GCACGTGCCACCACGCCTGACACATTTTTTAAATTTTTGTAGAGACAGTGTTTCAC
CATGTTGCCCAGGCAGGTCTCAAACTCCTGGGCTCAAGTGGTCCTCCAGCTTCAGC
10 CTCCCAAAGTGCTAGGATTATAGGTGTGAGCCACAGTGCCCAGCCCCGTAGTGGAG
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CAGAGGAGAAAGCACAGTGAAGAATGCAGTGTGTTCTGAGGTCCTGTCACCCCTGA
GGCTGTGTGTGTCCTTTGCCAAATTAAAGAGTCTTACTGAATGCGGTGCATCCAGG
AGACAGGCCNAGGTTTGGACTGGTAAAAAAAAA

15

Sequence ID 1399
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CATGTGACCCACCACCCCATCTNTGACCATGAGGCCACCCTGAGGTGCTGGGCCCT
GGGCTTCTACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGCGAGGACCAAA
20 CTCAGGACACCGAGCTTGTGGAGACCAGACCAGCAGGAGACAGAACCTTCCAGAAG
TGGGCAGCTGTGGTGGTGCCTTCTGGAGAAGAGCAGAGATACACATGCCATGTACA
GCATGAGGGGCTGCCGAAGCCCCTCACCCTGAGATGGGAGCCATCTTCCCAGTCCA
CCGTCCCCATCGTGGGCATTGTTGCTGGCCTGGCTGTCCTAGCAGTTGTGGTCATC
GGAGCTGTGGTCGCTGCTGTGATGTGTAGGAGGAAGAGTTCAGGTGGAAAAGGAGG
25 GAGCTACTCTCAGGCTGCGTCCAGCGACAGTGCCCAGGGCTCTGATGTGTCTCTCA
CAGCTTGAAAAGCCTGAGACAGCTGTNTTGTGAGGGACTGAGATGCAGGATTTCTT
CACGCCTCCCCTTTGTGACTTCAAGAGCCTCTGGCATCTCTTTCTGCAAAGGCACC
TGAATGTGTCTGCGTCCTTGTTAGCATAATGTGAGGAGGTGGAGAGACAGCCCACC
CTTGTGTCAACTGTGACCCCCTGTTCCCATGCTGACCTGTGTTTCCTCCCCAGTCA
30 TCTTTTTTGTTCNCAATAGGTGGGGCCTGGATGTCTCCATCTCTGTNTCA

Sequence ID 1440
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35 TTTCTTTATCCACTCATCAGTTGATGGGCATGTAGGTTGGTTCCATATCTTTGCAA
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GCACCTATTATACCAGGACTTTAAAAATCAGTCTGATAAGTCTTTGATAAGTCTAA

5   TAATAATAACTGATAAGTCCATTGAATTTGCTTCTGATTACTTTTTCTTTAGTAGC
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CGTTCCAGGTCAGTCAATATTAACTTCTTATAATTTTCTTTTTTTTCTTT

10   Sequence ID 1447
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AGGAGAGCCAAAGCTAAGACCCCCGAAACCAGACGAGCTACCTAAGAACAGCTAAA
AGAGCACACCCGTCTATGTAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACA
AACCTACCGAGCCTGGTGATAGCTGGTTGTCCAAGATAGAATCTTAGTTCAACTTT

15   AAATTTGCCCACAGAACCCTCTAAATCCCCTTGTAAATTTAACTGTTAGTCCAAAG
AGGAACAGCTCTTTGGACACTAGGAAAAAACCTTGTAGAGAGTAAAAAATTTAA
CACCCATAGTAGGCCTAAAAGCAGCCACCAATTAAGAAAGCGTTCAAGCTCAACAC
CCACTACCTAAAAAATCCCAAACATATAACTGAACTCCTCACACCCAATTGGACCA
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20   TCCGCATAAGCCTGCGTCAGATTAAAACACTGAACTGACAATTAACAGCCCAATAT
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TCATAAGGAAAGGT

Sequence ID 1448
25   GGCCACCGGGTGCAAGGTCAGGGCTGGGGTGGAGGCTGGGAAGCCCAGGGCTTGGC
CCACTGTGGCCGCCTTGTGTGGTCACTGCTTTCCTGGGCCTGCTGTGAGCTCCCTC
TAGGACCCCAGGCCTGTCTGGTGGGTCACTGTGACCACCACCTTGCACAGCACCTG
GCGCGTGGCAGGTGCTCAAACATTACTTGTTTCGGAATGAACTTCATCTTGCTCTT
GGCTTTTTGACTAATGCTGTGGAACATCTGACTAATTAGTGACTCTTTGGGGCCCC

30   CAGTTTCCCAGCTATAAAGTGGTAATATTAAGATAATAATTCGGCCGGGCGCGGTG
GCTCACGCCTGTAATCCCAGCAGCACTTTGGGAGGCCGAGGTGGGCAGATCACGAG
GTCAGAAGATCGAGACCATCCTGGCTAACACGGTGAAACCCCATCTCTACTAAAAA
TACAAAAAATTANCCGGGCGTGGTGGCGGGCGCCTGTAGTCCCAGCTACTCANGAG
GCTGANGCAGGAGAATGGTGTGAACCCGGGAGGCAGAGGTTGCAGTGAACCAAGAT

35   CGNNCCACTGCACTCCAGCCTGGGCAACAGAGCGAGACTCCATCTTAAAAAA

Sequence ID 1449

- 274 -

AATCAGGGCCGCAGTGTGTTCTGCGCCTGCCCAGAGCTGACTCCTGATTTAACCGC
TGGCGTAACCGCGGGTTGCACGCATGCGTGCTGAAAAGCCTTTCACCCTCACGTGG
TTTCTTTTTTAACCAGTCATCAAGCGAGGCTCGCGCGCAGGCCCCGCGTTGGAAAA
TGGCGGGGAAGCTGAAACCTCTGAATGTGGAGGCGCCAGAAGCTGCTGAGGAGGCT
GAAGGTAGTGAGGGCAAGTGGGCTGCACTCCTTTCTCTCCAACCAGGGCAGAAAGG
AGGGAGGATTCGTCCCATTACAATAATGAAATAATGATATTCTAATTTTTTTAAAT
AAAATGTTAAGCCTTTTGTTATTGAA

Sequence ID 1450

GGAAANCATGAGGCTTCGGGAGCCGCTCCTGAGCGGCAGCGCCGCGATGCCAGGCG
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GTCACCCTCGTTTACTACCTGGCTGGCCGCGACCTGAGCCGCCTGCCCCAACTGGT
CGGAGTCTCCACACCGCTGCAGGGCGGCTCGAACAGTGCCGCCGCCATCGGGCAGT
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TCCCAGCCGCGCCCGGGTGGCGACTCCAGCCCAGTCGTGGATTCTGGCCCTGGCCC
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CCTGCCCTGAGGAGTCCCCGCTGCTTGGTAAGGACTCGGGTCGGCGCCAGTCGGAG
GATTGGGACCCCCCGGATTTCCCCGACAGGGTCCCCCANACATTCCCTCAGGCTG
GCTCTTCTACGACAGCCAGCCTCCCTCTTCTGGATCAGAGTTTTAAATCCCANACA
GAGGCTTGGGACTGGATGGGAGAGAAGGTTTGCGAGGTGGGTCCCTGGGGAGTCCT
GTTGGAGGCGTGGGGCCGGGACCGCACAGGGAAGTCCCGAGGCCCCTCTAGCCCCA
AAACCANAGAAGGCCTTGGAGACTTCCCTGCTGTGGCCCGAGGCTNAGGAAGTTTT
GGAGTTTTGGGTCTGCTTANGGCTTCNAGCAGCCTTGCACTGAGAACTTTGGTAGG
GACCTCGAGTAATCCACTCCNTTTTNGGGACTGACGTGAGGCTCCCGGTGGGGAAA
GANACTGACCTNTC

Sequence ID 1453

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TTGAAGTTGACTTACTGAAGAATGGAGAGAGAATTGAAAAAGTGGAGCATTCAGAC
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CACTGAAAAAGATGAGTATGCCTGCCGTGTGAACCATGTGACTTTGTCACAGCCCA
AGATAGTTAAGTGGGATCGAGACATGTAAGCAGCATCATGGAGGTTTGAAGATGCC
GCATTTGGATTGGATGAATTCCAAATTCTGCTTGCTTGCTTTTTAATATTGATATG
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CATGATCTTCTTTATAATTCTACTTTGAGTGCTGTCTCCATGTTTGATGTATCTGA

GCAGGTTGCTCCACAGGTAGCTCTAGGAGGGCTGGCAACTTAGAGGTGGGGAGCAG
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GCACTCAAAGCTTGTTAAGATAGTTAAGCGTGCATAAGTTAACTTCCAATTTACAT
ACTCTGCTTAGAATTTGGGGGAAAATTTAGAAATATAATTGACAGGATTATTGGAA
ATTTGTTATAATGAATGAAACATTTTTGTCATATAAGATTCATATTTACTTCTTAT
ACA

Sequence ID 1454
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TTGGAACCAACCCAAATGTCCAACAATGATAGACCGGGTTAAGAAAATGCGGCACA
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GGGACATGGATGAAATTGGAAATCATCATTCTCAGTAAACTATCGCAGGAACAAAA
AACCAAACACTGCATATTCTCACTCATAGGTGGGAATTGAACAGTGGGAACACATG
GACACAGGAAGGGGAACATCACACTCTGAGGACTGTTGTGGGGTGGGGGGAGGGAG
GAGGGATAGCATTGGGAGATATACCTAGTGCTGGATGACGAGTTAGTGGGTGCAGC
GCACCAGCATGTCACATGTATACATATGTAACTAACCTGCACATTGTGCACATGTA
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Sequence ID 1456

CCGCAACAAACACGGGAGTGCAGATATCGCTGCGATGGGCTGATTTCCTTTATTTG
GGTATATACCCAGCAGTGGGATTGCTGGATTGTATGGTAGCTCTATTAGTTTTTTG
AGGAACCTCCAAACTGTTCTNCATAGTGGTTGTACTCATTTACATTCCCACTGTGA
ACCCTGAAAATTTGAGGCAGGTCTCAGTTAAATTAGAAAGTTGATTTTGCCAAGTT
GGGGACACGCACTCGTGACACAGCCTCAGGAGGAACTGATGACATGTGCCCAGGTG
GTCAGAGCACAGCTTGGTTTTATACATTTTAGGGAAACCTGAGCCATCAATCAACA
TACGTAAAATGGGCCGGGCACAGCAGCTCAAGCTGTAATCCCAGCACTCTGGGAGG
CCGAGGCGGGTGGATCACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGG
TGAAACCCCGTCTCTATTAAAAATACAAAGCTTAGCTGGATGTGGTGGCGCATGCC
TGTAGTCCCAGCTGCTCTAGGAGGCTGAGGCATGAGAATTGCTTGAACCTGGGAGG
CAGAGGCTGCAGTGAGCCGAGATCGAGCCACTATACTCCAGCCTGGTCAACAGAGT
GAGACCCTGTCT

Sequence ID 1460
CCACAACTGTGTTCACTAGCAACCTCAAACAGACACCATGGTGCACCTGACTCCTG

AGGAGAAGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAAGTTGGT
GGTGAGGCCCTGGGCAGGCTGCTGGTGGTCTACCCTTGGACCCAGAGGTTCTTTGA
GTCCTTTGGGGATCTGTCCACTCCTGATGCTGTTATGGGCAACCCTAAGGTGAAGG
CTCATGGCAAGAAAGTGCTCGGTGCCTTTAGTGATGGCCTGGCTCACCTGGACAAC
CTCAAGGGCACCTTTGCCACACTGAGTGAGCTGCACTGTGACAAGCTGCACGTGGA
TCCTGAGAACTTCAGGCTCCTGGGCAACGTGCTGGTCTGTGTGCTGGCCCATCACT
TTGGCAAAGAATTCACCCCACCAGTGCAGGCTGCCTATCAGAAAGTGGTGGCTGGT
GTGGCTAATGCCCTGGCCCACAAGTATCACTAAGCTCGCTTTCTTGCTGTCCAATT
TCTATTAAAGGTTCCTTTGTTCCCTAAGTCCAACTACTAAACTGGGGGATATTATG
AAGGGCCTTGAGCATCTGGATTCTGCCTAATAAAAACATTTATTTTCATTG

Sequence ID 1490

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GCCCTACCACAAGAAGCGGAAGTATGAGTTGGGGCGCCCAGCTGCCAACACCAAGA
TTGGCCCCCGCCGCATCCACACAGTCCGTGTGCGGGGAGGTAACAAGAAATACCGT
GCCCTGAGGTTGGACGTGGGGAATTTCTCCTGGGGCTCANAGTGTTGTACTCGTAA
AACAAGGATCATCGATGTTGTCTACAATGCATCTAATAACGAGCTGGTTCGTACCA
AGACCCTGGTGAAGAATTGCATCGTGCTCATCGACAGCACACCGTACCGACAGTGG
TACGAGTCCCACTATGCGCTGCCCCTGGGCCGCAAGAAGGGAGCCAAGCTGACTCC
TGAGGAAGAAGAGATTTTAAACAAAAAACGATCTAAAAAAATTCAGAAGAAATATG
ATGAAAGGAAAAGAATGCCAAAATCAGCAGTCTCCTGGAGGAGCAGTTCCAGCAG
GGCAAGCTTCTTGCGTGCATCGCTTCAAGGCCGGGACAGTGTGGCCGAGCAGATGG
CTATGTGCTAGAGGGCAAAGAGTTGGAGTTCTATCTTAGGAAAATCAAGGCCCGCA
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TTGTT

Sequence ID 1491

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GCCCCAACCACCTTGGGNACATGTGGNGAGGACCTCCTGAGGCTGTGTCATGGGCA
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CTTAAAATCATGTGTAGAAGTAGCCTGTGATATAGTCCTAGATACATACATTATCA
TCTTATGTATCTTCCCTCCCTCTTCCAGGTTCTGATAAAAACAGATGAAATCTGAA
AGACCATGACAGTAGTATTTTGAAAATGACAGTATTTGAAATTAAAAAATTGTAAA
AGTGTTCTGTTCTATCACTGCCAAAGGATAAGTTACAAATTGGTTCTTGGAACGTA
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GACTAATTTTACCTTTTTTTAACCTATGACTCTTTAGTTATAGTAGTACAAAAAAG

- 277 -

TAGTTTTAGTTATAGTTTTAGTTGTAGTACAAAAAAGCATTTTCTGTAAGCTTAAT
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AATATGTT

5

Sequence ID 1492
TGTNCCTGTAGTCCTGTGTGGGAGGATTGCCTGAGCCTAGGAGCTCAAAGTTGCAG
TGAGCCCAGATCGNGNCATTGCAGTCCAGCCTGGGTGACAGAGTGAGACCCCATGT
CAAAAAAAAAAAAACAAAAAACAGGGGCCTGCCTCANCCAGCAGGTGAGGTCTGCC
10   ACTGAGAGCACTTCTAGCAGCAGGAACAGCCTCCACCCCCACACTGCAATCAAGTT
TTTTGGGTCAGCCTTAGGAGCTAANAAAGGGCCTAGTTTGNCTAAATAGCAGGAGT
TATATCCAGGGATCTTCAGGCCCAGGAATGCTAATGAGTAGGCATTCCATGGGCCC
TGGGAATGGCTTTGTGTGCCANAAATGATGGCCACAAAGGCCTTGCTGCCTTTTTT
CAAAATGGCTGCATCCAGCTGAGTGCTCTCTGCCAAAGGGGANAANAAAATAAGTC
15   TCCAGTGCATTTAGATTGGTCTCTCATCATCTCTCTCCTTTTTGTTTTTATTAGTC
TCCTTAACCAAAACTGCCAAGAAAGGCTTGGAATTGAAACAAAACCTGATANAANA
GGTAAGAGGTTGTTCTTTT

Sequence ID 1493
20   TGTNTCAAAAAAAAAAAAAAAGAACGGNAATGTACTGGAGATGTATTTGATAACCAA
GGNTTTAGGTAAATTTTCACCAGTATTAGTTNTATTTGCAAACTGAAAAATGTTGT
AGGCTTAATATAAAATAACCACATTAGTGAACATTATATCTCTTAGAAGAAAGGCC
ATATTTTGCTCCTGCTTCTGTAAAAATATTATTTGTTTGAAGGGGAAATAATGGTA
GTGTGACCTTTCACTTAATTCCTACTCCCTTAATGTGAGAGAGACAAAATGAGCTG
25   AAGAAGGAAAATTCTGGAGTTACACTCCACAACCTTGAACATACTGACGGACATCT
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GACAACCCTCTTTGCACAAGCTACAGCATCAGCGATGTTATCTTGCAGCAAAGCAC
TGCAGGATAAATGACAGGCATTAACTGCTCCTGGGGTTTTGCCATCATTACACCAG
TAGCGGCTATTGATCTGAAATATCCCATAATCAGTGCTTCTGTCTCCAGCATTGTA
30   GTTTGTAGCTCGTGTGTTGTAACCACTCTCCCATTTGGCCAAACACATCCAGTTTG
CTAGGCTGATTCCCCTGTAGCCATCCATTCCCAATCTTTTCAGAGTTCTGGCCAAC
TCACACCTTTCAAAGACCTTGCCCTGGACCGTAACAGAAAGGAGGACAAGCCCCAG
AACAATGAGAGCCTTCATGTTGAC

35   Sequence ID 1494
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CCCAGGAGTTCAGGACCAGCCTGGGCAGCATACCGGGATTCCATCTNNACTAAAAA

CAGTAGGCTGGGTGTGGTGGCTCATGTCTGTAAGCTCAGGACTTTGGAAGGCCAAG
ATGGGAGGATCACTTGAGCCTGGGAGTTTGACACCAGCTTGAGCATCGTAGCCAGG
CCCTGACTCTACAAAAAAGTGAAATAATTAGCCGAGTGTGGTGGTTCACACCTGTA
ATCCCAGCTGCTCAGGAGGCTGAGGTAGGAGAATCATTTGAACCCGGGAGGTGGAG
GTTGCAGTTAGCCGAGATCACGCCATTGCACTCCGGCCTGGGCGATAAAGCGAGAC
TCTGTCTCAAAAAAAAAAAAAA

Sequence ID 1495

ATTCGGGCCGAGATGTCTCGCTCCGTGGCCTTAGCTGTGCTCGCGCTACTCTCTCT
TTCTGGCCTGGAGGCTATCCAGCGTACTCCAAAGATTCAGGTTTACTCACGTCATC
CAGCAGAGAATGGAAAGTCAAATTTCCTGAATTGCTATGTGTCTGGGTTTCATCCA
TCCGACATTGAAGTTGACTTACTGAAGAATGGAGAGAGAATTGAAAAAGTGGAGCA
TTCAGACTTGTCTTTCAGCAAGGACTGGTCTTTCTATCTCTTGTACTACACTGAAT
TCACCCCCACTGAAAAAGATGAGTATGCCTGCCGTGTGAACCATGTGACTTTGTCA
CAGCCCAAGATAGTTAAGTGGGATCGAGACATGTAAGCAGCATCATGGAGGTTTGA
AGATGCCGCATTTGGATTGGATGAATTCCAAATTCTGCTTGCTTGCTTTTTAATAT
TGATATGCTTATACACTTACACTTTATGCACAAAATGTAGGGTTATAATAATGTTA
ACATGGACATGATCTTCTTTATAATTCTACTTTGAGTGCTGTCTCCATGTTTGATG
TATCTGAGCAGGTTGCTCCACAGGTAGCTCTAGGAGGGCTGGCACCTTAGAGGTGG
GGAGCAGAGAATTCTCTTATCCAACATCAACATCTTGGTCAGATTTGAACTCTT

Sequence ID G6

GGATTTTTGGTCCGCACGCTCCTGCTCCTGACTCACCGCTGTTCGCTCTCGCCGAG
GAACAAGTCGGTCAGGAAGCCCGCGCGCAACAGCCATGGCTTTTAAGGATACCGGA
AAAACACCCGTGGAGCCGGAGGTGGCAATTCACCGAATTCGAATCACCCTAACAAG
CCGCAACGTAAAATCCTTGGAAAAGGTGTGTGCTGACTTGATAAGAGGCGCAAAAG
AAAAGAATCTCAAAGTGAAAGGACCAGTTCGAATGCCTACCAAGACTTTGAGAATC
ACTACAAGAAAAACTCCTTGTGGTGAAGGTTCTAAGACGTGGGATCGTTTCCAGAT
GAGAATTCACAAGCGACTCATTGACTTGCACAGTCCTTCTGAGATTGTTAAGCAGA
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TAAGTCAACTATTTTAATAAATTGATGACCAGTTGTTAAAA

Sequence ID - 61   nt: 362
CTTATTGAAAATTTTACTAATTTCTTACTTTTTAGGTTTTAGGAGAATACTTTTGGA
TAATTGACTAGCCTCACATTATATTGATAGAGGTTCTTGAAAACTTTAATGCCAAT
TCATGTATCTTATGACTAAAATAGATAATCCATTTAGAAATTTAAGTCATTCTTGC
GTGCTTGATATGTGTCAGCACTATCCAAGTTGCTAGGGGATACAATGGTGAAGTG
AAAATATCAGCTAGGTGCCGGTGGCTCACACCTGTTATCCCAACAGTTTGGGAGG
CCAGGGTGGGAGGATCACTCAAGCACANGCGTTTCACACCAGCCTGGACAACAT
ACAAGACCCCATCTTTACCAAAAGTTAAG

Sequence ID - 490   nt: 382

TTTTCTTAGAACTTTATTTTTTCTGGCCAGGCGCAGTGGCTCACACCTGTAATCCC
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AGCCTGGCCAACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCTGG
GCGTGGTGGCGCATGCCTGTAATCCCANCTACTCAGGAGGCTGAGGCAGGAGAA
TTGTTTGAACCCGGGAGGCGGAGGTTGCANTGAGCCGAGATTGCGCCACTGCACT
CCAGCCTGGGCAACAGAGCGAAACTCCATCTCAAAAAAAAAAAAAAAAAAACAAC
CTTTATTTTTTCTGATTTTAAAAGTAATAACTAGTTTGTAGAAACATTAAAAGT

Sequence ID - 892   nt: 559
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GGTCGTAAGGGCTGAGGATTTTTGGTCCGCACGCTCCTGCTCCTGACTCACCGCT
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GCTTTTAAGGATACCGGAAAAACACCCGTGGAGCCGGAGGTGGCAATTCACCGA
ATTCGAATCACCCTAACAAGCCGCAACGTAAAATCCTTGGAAAAGGTGTGTGCTG
ACTTGATAAGAGGCGCAAAAGAAAAGAATCTCAAAGTGAAAGGACCAGTTCGAA
TGCCTACCAAGACTTTGAGAATCACTACAAGAAAAACTCCTTGTGGTGAAGGTTC
TAAGACGTGGGATCGTTTCCAGATGAGAATTCACAAGCGACTCATTGACTTGCAC
AGTCCTTCTGAGATTGTTAAGCAGATTACTTCCATCAGTATTGAGCCAGGAGTTG
AGGTGGAAGTCACCATTGCAGATGCTTAAGTCAACTATTTTAATAAATTGATGAC
CAGTTGTTT

Sequence ID - 77   nt: 464
GCGGCTGCTGTTGGTTGGGGGCCGTCCCGCTCCTAAGGCAGGAAGATGGTGGCCG
CAAAGAAGACGAAAAAGTCGCTGGAGTCGATCAACTCTAGGCTCCAACTCGTTAT
GAAAAGTGGGAAGTACGTCCTGGGGTACAAGCAGACTCTGAAGATGATCAGACA
AGGCAAAGCGAAATTGGTCATTCTCGCTAACAACTGCCCAGCTTTGAGGAAATCT
GAAATAGAGTACTATGCTATGTTGGCTAAAACTGGTGTCCATCACTACAGTGGCA
ATAATATTGAACTGGGCACAGCATGCGGAAAATACTACAGAGTGTGCACACTGG
CTATCATTGATCCAGGTGACTCTGACATCATTAGAAGCATGCCAGAACAGACTGG
TGAAAAGTAAACCTTTTCACCTACAAAATTTCACCTGCAAACCTTAAACCTGCAA
AATTTTCCTTTAATAAAATTTGCTTG

- 280 -

Claims:

1.   A set of oligonucleotide probes, wherein said set comprises at least 10 oligonucleotides selected from: an oligonucleotide as described in Table 1 or derived from a sequence described in Table 1, or an oligonucleotide with a complementary sequence, or a functionally equivalent oligonucleotide.

2.   A set of oligonucleotide probes as claimed in claim 1 wherein said oligonucleotide probes are selected from: an oligonucleotide as described in Table 2 or derived from a sequence described in Table 2, or an oligonucleotide with a complementary sequence, or a functionally equivalent oligonucleotide.

3.   A set of oligonucleotide probes as claimed in claim 1 wherein said oligonucleotide probes are selected from: an oligonucleotide as described in Table 4 or derived from a sequence described in Table 4, or an oligonucleotide with a complementary sequence, or a functionally equivalent oligonucleotide.

4.   A set of oligonucleotide probes as claimed in any one of claims 1 to 3, wherein each probe in said set binds to a different transcript.

5.   A set as claimed in any one of claims 1 to 4 consisting of from 10 to 500 oligonucleotide probes.

6.   An oligonucleotide probe wherein said probe is selected from the oligonucleotides listed in Table 1, or derived from a sequence described in Table 1, or a complementary sequence thereof.

7.   A set of oligonucleotide probes as claimed in any one of claims 1 to 5, or an oligonucleotide probe as

- 281 -

claimed in claim 6, wherein each of said oligonucleotide probes is from 15 to 200 bases in length.

8.   A set of oligonucleotide probes as claimed in any one of claims 1 to 5 or 7 or an oligonucleotide probe as claimed in claim 6 or 7, wherein the transcript to which said probe binds is derived from a gene which is constitutively moderately or highly expressed.

9.   A set of oligonucleotide probes as claimed in any one of claims 1 to 5, 7 or 8 or an oligonucleotide probe as claimed in any one of claims 6 to 8, wherein said probes are immobilized on one or more solid supports.

10.   A set of oligonucleotide probes or an oligonucleotide probe as claimed in claim 9, wherein said solid support is a sheet, filter, membrane, plate or biochip.

11.   A polypeptide encoded by the mRNA sequence to which an oligonucleotide as defined in claim 6 binds.

12.   An antibody to a polypeptide as defined in claim 11.

13.   A kit comprising a set of oligonucleotide probes immobilized on one or more solid supports as defined in claim 9 or 10.

14.   A kit as claimed in claim 13 wherein said probes are immobilized on a single solid support and each unique probe is attached to different region of said solid support.

15.   A kit as claimed in claim 13 or 14 further comprising standardizing materials.

16. The use of a set of probes as described in any one of claims 1 to 5 or 7 to 10 or a kit as described in any one of claims 13 to 15 to determine the gene expression pattern of a cell which pattern reflects the level of gene expression of genes to which said oligonucleotide probes bind, comprising at least the steps of:

a) isolating mRNA from said cell, which may optionally be reverse transcribed to cDNA;

b) hybridizing the mRNA or cDNA of step (a) to a set of oligonucleotides or a kit as defined in any one of claims 1 to 5, 7 to 10 or 13 to 15; and

c) assessing the amount of mRNA or cDNA hybridizing to each of said probes to produce said pattern.

17. A method of preparing a standard gene transcript pattern characteristic of a disease or condition or stage thereof in an organism comprising at least the steps of:

a) isolating mRNA from the cells of a sample of one or more organisms having the disease or condition or stage thereof, which may optionally be reverse transcribed to cDNA;

b) hybridizing the mRNA or cDNA of step (a) to a set of oligonucleotides or a kit as defined in any one of claims 1 to 5, 7 to 10 or 13 to 15 specific for said disease or condition or stage thereof in an organism and sample thereof corresponding to the organism and sample thereof under investigation; and

c) assessing the amount of mRNA or cDNA hybridizing to each of said probes to produce a characteristic pattern reflecting the level of gene expression of genes to which said oligonucleotides bind, in the sample with the disease, condition or stage thereof.

18. A method of preparing a test gene transcript pattern comprising at least the steps of:

a) isolating mRNA from the cells of a sample of

said test organism, which may optionally be reverse
transcribed to cDNA;

     b) hybridizing the mRNA or cDNA of step (a) to a
set of oligonucleotides or a kit as defined in any one
of claims 1 to 5, 7 to 10 or 13 to 15 specific for a
disease or condition or stage thereof in an organism and
sample thereof corresponding to the organism and sample
thereof under investigation; and

     c) assessing the amount of mRNA or cDNA hybridizing
to each of said probes to produce said pattern
reflecting the level of gene expression of genes to
which said oligonucleotides bind, in said test sample.

19.   A method of diagnosing or identifying or monitoring
a disease or condition or stage thereof in an organism,
comprising the steps of:

     a)   isolating mRNA from the cells of a sample of
         said organism, which may optionally be reverse
         transcribed to cDNA;

     b)   hybridizing the mRNA or cDNA of step (a) to a
         set of oligonucleotides or a kit as defined in
         any one of claims 1 to 5, 7 to 10 or 13 to 15
         specific for said disease or condition thereof
         in an organism and sample thereof
         corresponding to the organism and sample
         thereof under investigation;

     c)   assessing the amount of mRNA or cDNA
         hybridizing to each of said probes to produce
         a characteristic pattern reflecting the level
         of gene expression of genes to which said
         oligonucleotides bind in said sample; and

     d)   comparing said pattern to a standard
         diagnostic pattern prepared as described in
         claim 17 using a sample from an organism
         corresponding to the organism and sample under
         investigation to determine the degree of
         correlation indicative of the presence of said

disease or condition or a stage thereof in the organism under investigation.

20.	A method as claimed in any one of claims 17 to 19 wherein said mRNA or cDNA is amplified prior to step b).

21.	A method as claimed in any one of claims 17 to 20 wherein the oligonucleotides and/or the mRNA or cDNA are labelled.

22.	A method as claimed in any one of claims 17 to 21 wherein said probes are as defined in claim 3 and said disease is Alzheimer's disease.

23.	A method as claimed in any one of claims 17 to 21 wherein said probes are as defined in claim 2 and said disease is breast cancer.

24.	A method as defined in any one of claims 17 to 23, wherein said set of oligonucleotides as defined in any one of claims 1 to 5, 7 to 10 or 13 to 15 are replaced with a set of oligonucleotides which are randomly selected, preferably from a cDNA library.

25.	A method of preparing a standard gene transcript pattern characteristic of a disease or condition or stage thereof in an organism comprising at least the steps of:

a) releasing target polypeptides from a sample of one or more organisms having the disease or condition or stage thereof;

b) contacting said target polypeptides with one or more binding partners, wherein each binding partner is specific to a marker polypeptide (or a fragment thereof) encoded by the gene to which an oligonucleotide of Table 1 (or derived from a sequence described in Table 1) binds, to allow binding of said binding partners to said

target polypeptides, wherein said marker polypeptides
are specific for said disease or condition thereof in an
organism and sample thereof corresponding to the
organism and sample thereof under investigation; and

5   c) assessing the target polypeptide binding to said
binding partners to produce a characteristic pattern
reflecting the level of gene expression of genes which
express said marker polypeptides, in the sample with the
disease, condition or stage thereof.

10

26. A method of preparing a test gene transcript
pattern comprising at least the steps of:
      a) releasing target polypeptides from a sample of
said test organism;

15   b) contacting said target polypeptides with one or
more binding partners, wherein each binding partner is
specific to a marker polypeptide (or a fragment thereof)
encoded by the gene to which an oligonucleotide of Table
1 (or derived from a sequence described in Table 1)

20   binds, to allow binding of said binding partners to said
target polypeptides, wherein said marker polypeptides
are specific for said disease or condition thereof in an
organism and sample thereof corresponding to the
organism and sample thereof under investigation; and

25   c) assessing the target polypeptide binding to said
binding partners to produce a characteristic pattern
reflecting the level of gene expression of genes which
express said marker polypeptides, in said test sample.

30   27.   A method of diagnosing or identifying or
monitoring a disease or condition or stage thereof in an
organism comprising the steps of:
      a) releasing target polypeptides from a sample of
said organism;

35   b) contacting said target polypeptides with one or
more binding partners, wherein each binding partner is
specific to a marker polypeptide (or a fragment thereof)

encoded by the gene to which an oligonucleotide of Table 1 (or derived from a sequence described in Table 1) binds, to allow binding of said binding partners to said target polypeptides, wherein said marker polypeptides are specific for said disease or condition thereof in an organism and sample thereof corresponding to the organism and sample thereof under investigation; and

c) assessing the target polypeptide binding to said binding partners to produce a characteristic pattern reflecting the level of gene expression of genes which express said marker polypeptides in said sample; and

d) comparing said pattern to a standard diagnostic pattern prepared as described in claim 25 using a sample from an organism corresponding to the organism and sample under investigation to determine the degree of correlation indicative of the presence of said disease or condition or a stage thereof in the organism under investigation.

28. A method as claimed in any one of claims 17 to 27 wherein said pattern is expressed as an array of numbers relating to the expression level associated with each probe.

29. A method as claimed in any one of claims 17 to 28 wherein said organism is a eukaryotic organism, preferably a mammal.

30. A method as claimed in claim 29 wherein said organism is a human.

31. A method as claimed in any one of claims 17 to 30 wherein the data making up said pattern is mathematically projected onto a classification model.

32. A method as claimed in any one of claims 17 to 31 wherein said disease is cancer or a degenerative brain

disorder.

33.   A method as claimed in any one of claims 17 to 32 wherein said sample is tissue, body fluid or body waste.

34.   A method as claimed in any one of claims 17 to 33 wherein said sample is peripheral blood.

35.   A method as claimed in any one of claims 17 to 34 wherein the cells in the sample are not disease cells, have not been in contact with such cells and do not originate from the site of the disease or condition.

36.   A method as claimed in any one of claims 19 to 35 for the diagnosis, identification or monitoring of two or more diseases, conditions or stages thereof in an organism, wherein said pattern produced in step c) is compared to at least two standard diagnostic patterns prepared as described in claim 17 or 25, wherein each standard diagnostic pattern is a pattern generated for a different disease or condition or stage thereof.

37.   A method of identifying probes useful for diagnosing or identifying or monitoring a disease or condition or stage thereof in an organism, comprising the steps of:

a)   immobilizing a set of oligonucleotide probes, preferably as described hereinbefore, on a solid support;

b)   isolating mRNA from a sample of a normal organism (normal sample), which may optionally be reverse transcribed to cDNA;

c)   isolating mRNA from a sample from an organism, corresponding to the sample and organism of step (b), which is known to have said disease or condition or a stage thereof (diseased sample), which may optionally be reverse
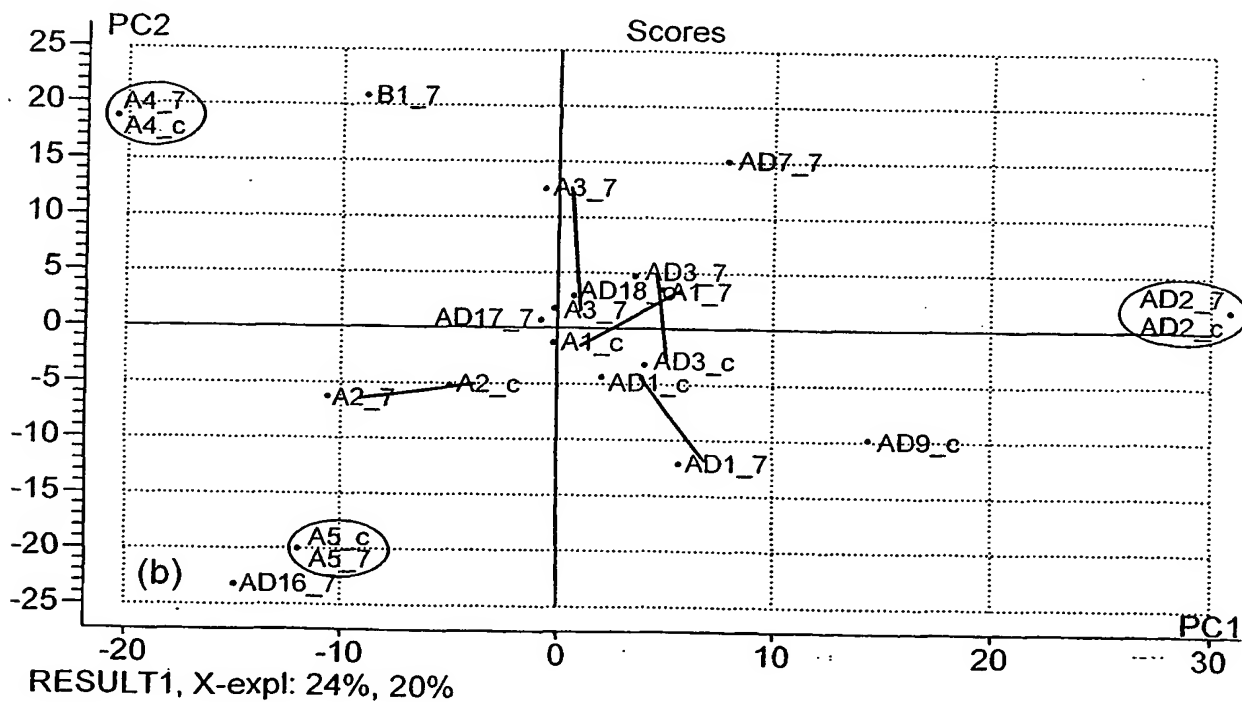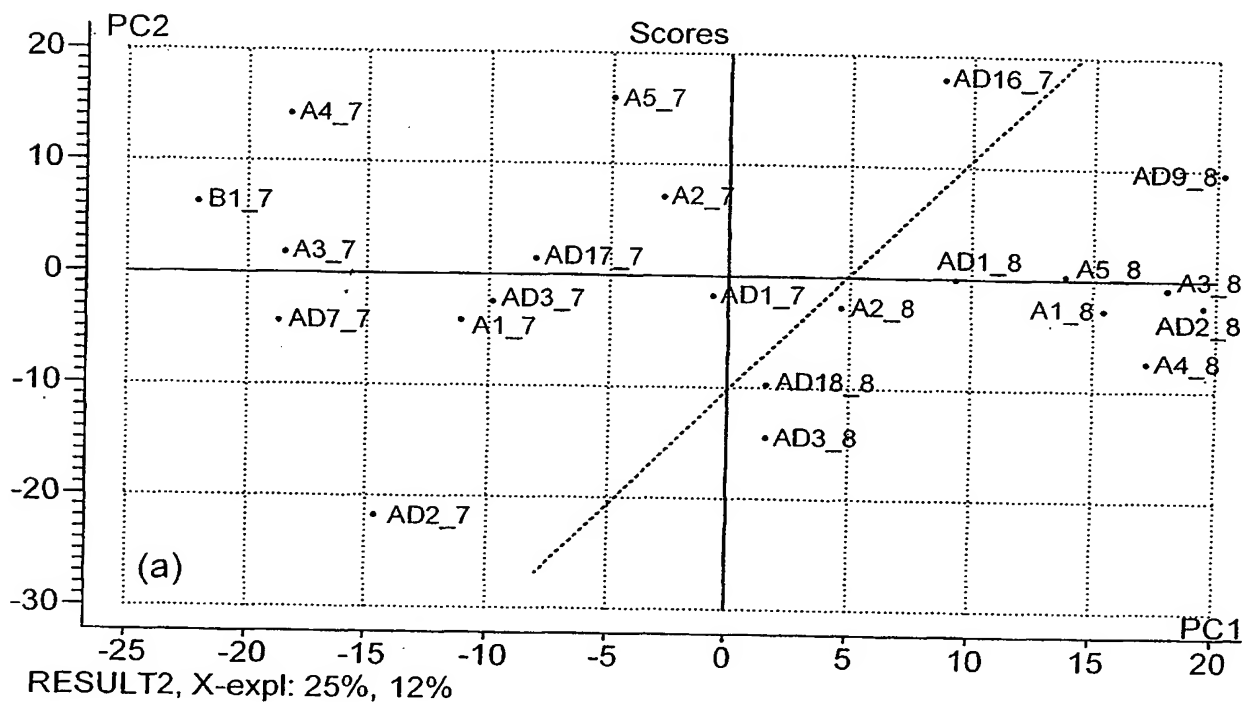
transcribed to cDNA;

d) hybridizing the mRNA or cDNA of steps (b) and (c) to said set of immobilized oligonucleotide probes of step (a); and

e) assessing the amount of mRNA or cDNA hybridizing to each of said oligonucleotide probes to determine the level of gene expression of genes to which said oligonucleotide probes bind in said normal and diseased samples to generate a gene expression data set for each sample;

f) normalizing and standardizing said data set of step (e);

g) constructing a calibration model for classification, preferably using the statistical techniques Partial Least Squares Discriminant Analysis (PLS-DA) and Linear Discriminant Analysis (LDA);

h) performing JackKnife analysis and identifying those oligonucleotide probes which are required for classification of said disease and normal samples into their respective groups.

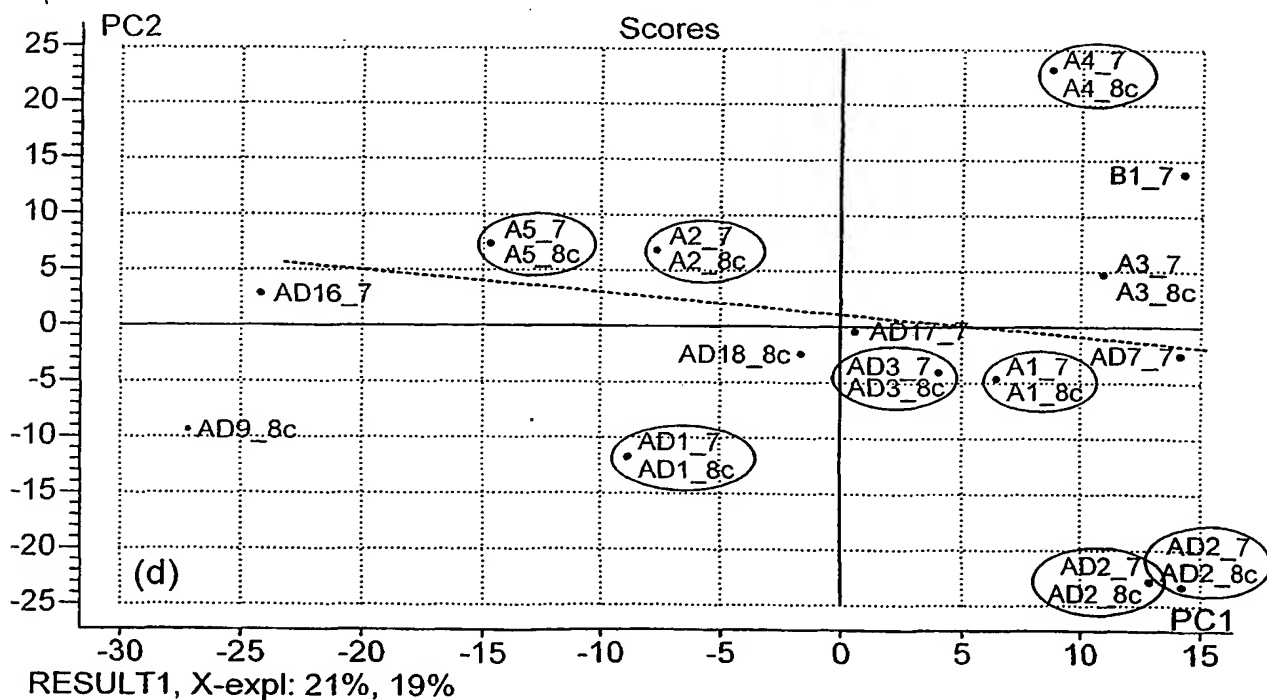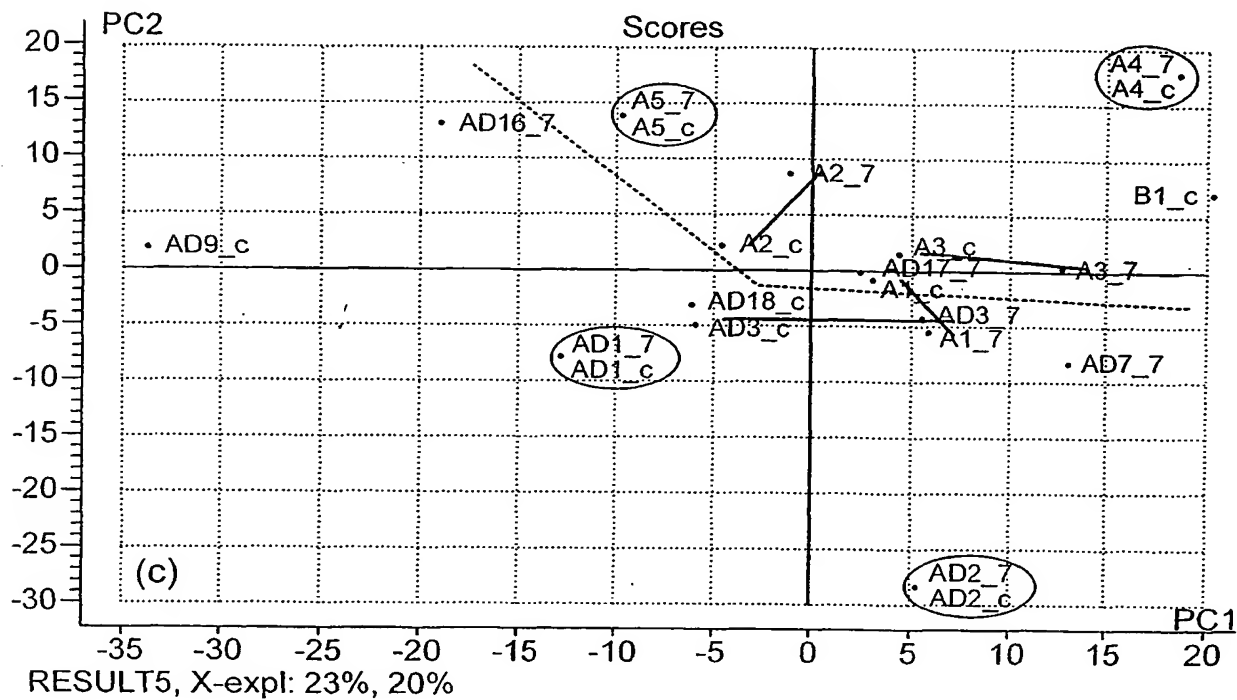Praveen SHARMA et al
PRODUCT AND METHOD
Q-87920

10/535414

WO 2004/046382   PCT/GB2003/005102

1 / 12

FIG. 1

Effect of Direct Standardization (DS) on the Alzheimer Data measured in two different series of experiments

(a) RESULT2, X-expl: 25%, 12%
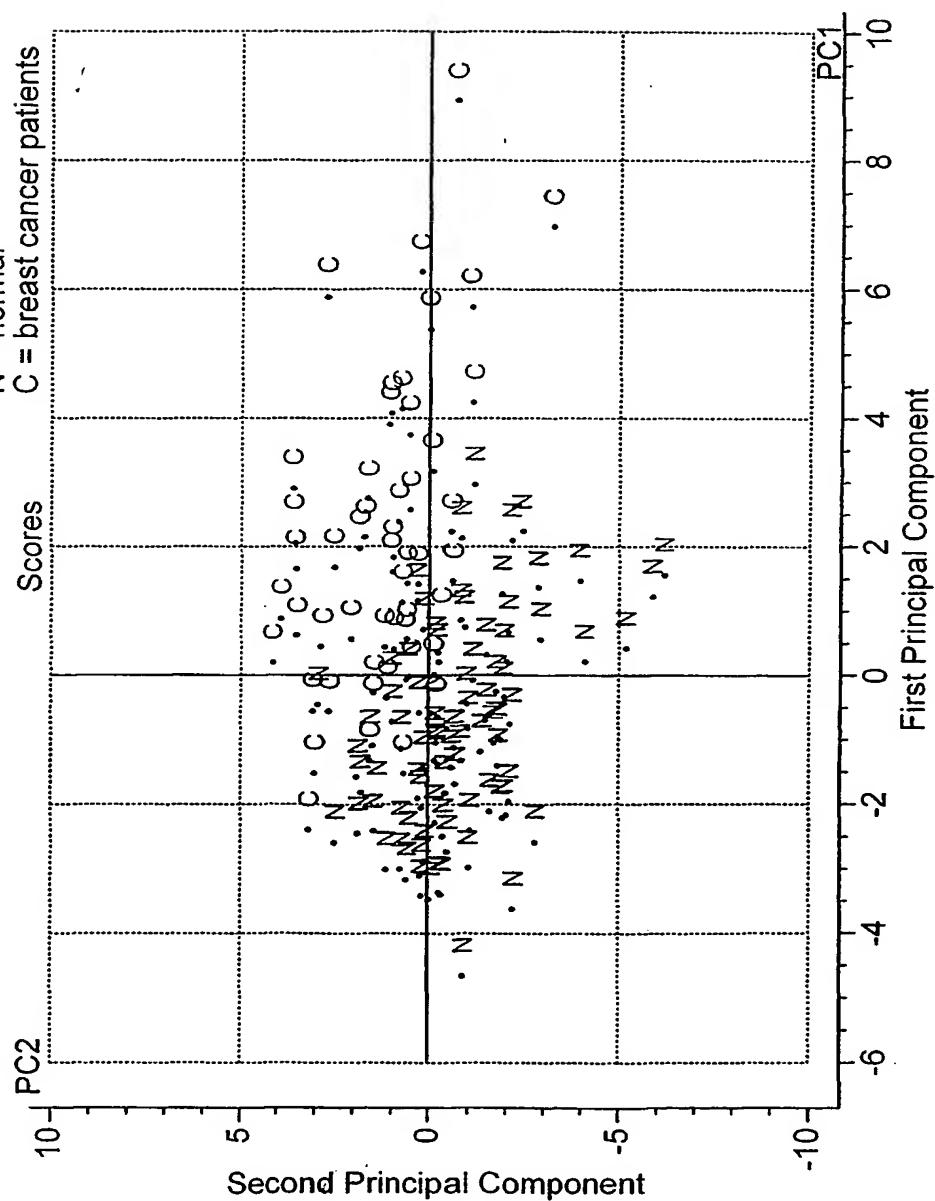
(b) RESULT1, X-expl: 24%, 20%

Praveen SHARMA et al
PRODUCT AND METHOD
Q-87920

WO 2004/046382

10/535414

PCT/GB2003/005102

2 / 12

FIG. 1 CONT'D

(c) RESULT5, X-expl: 23%, 20%

(d) RESULT1, X-expl: 21%, 19%

3 / 12

FIG. 2

Projection of normal (including benign) and breast cancer samples onto a
classification model generated by PLSR-DA using the data of 44 informative genes

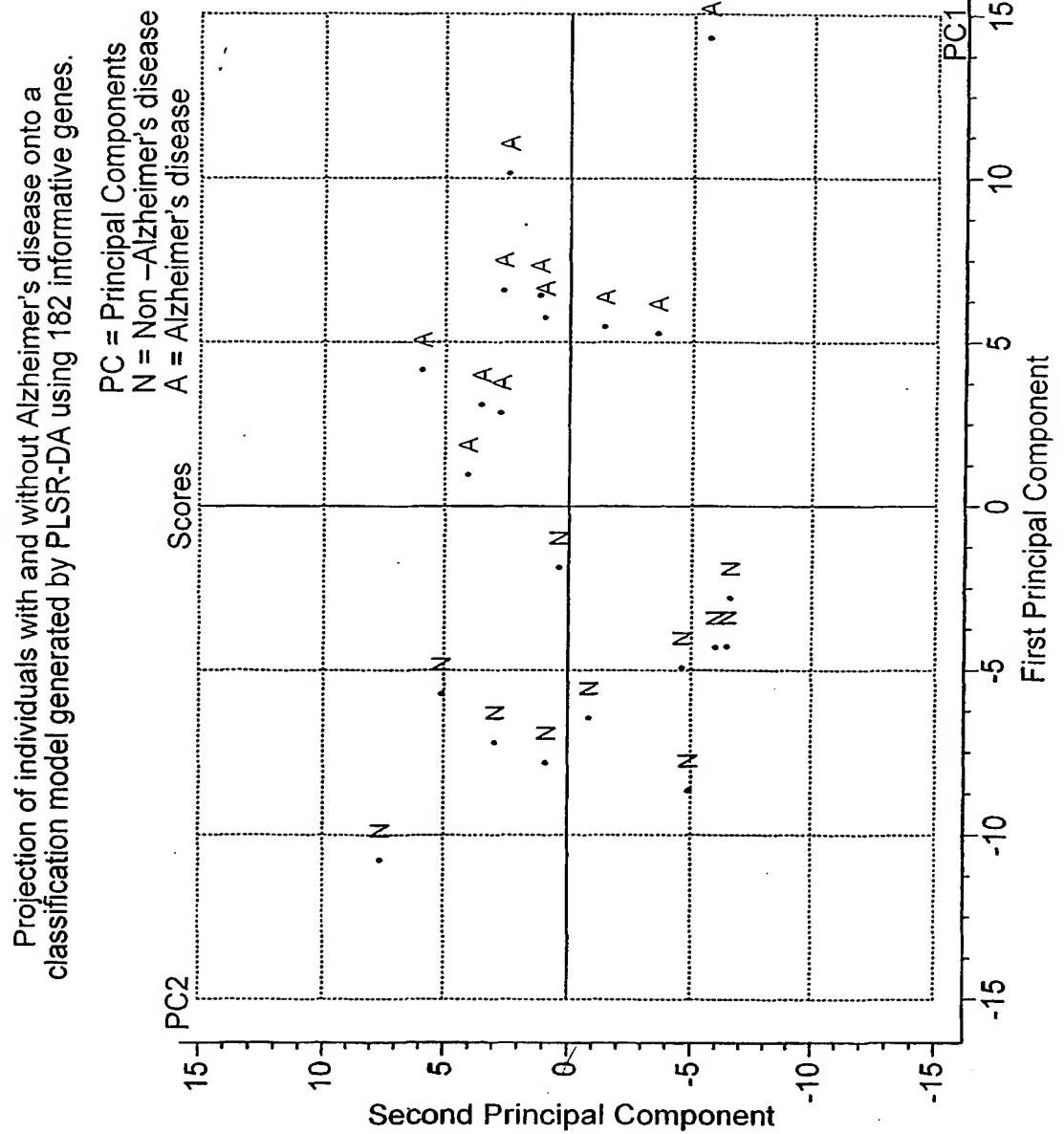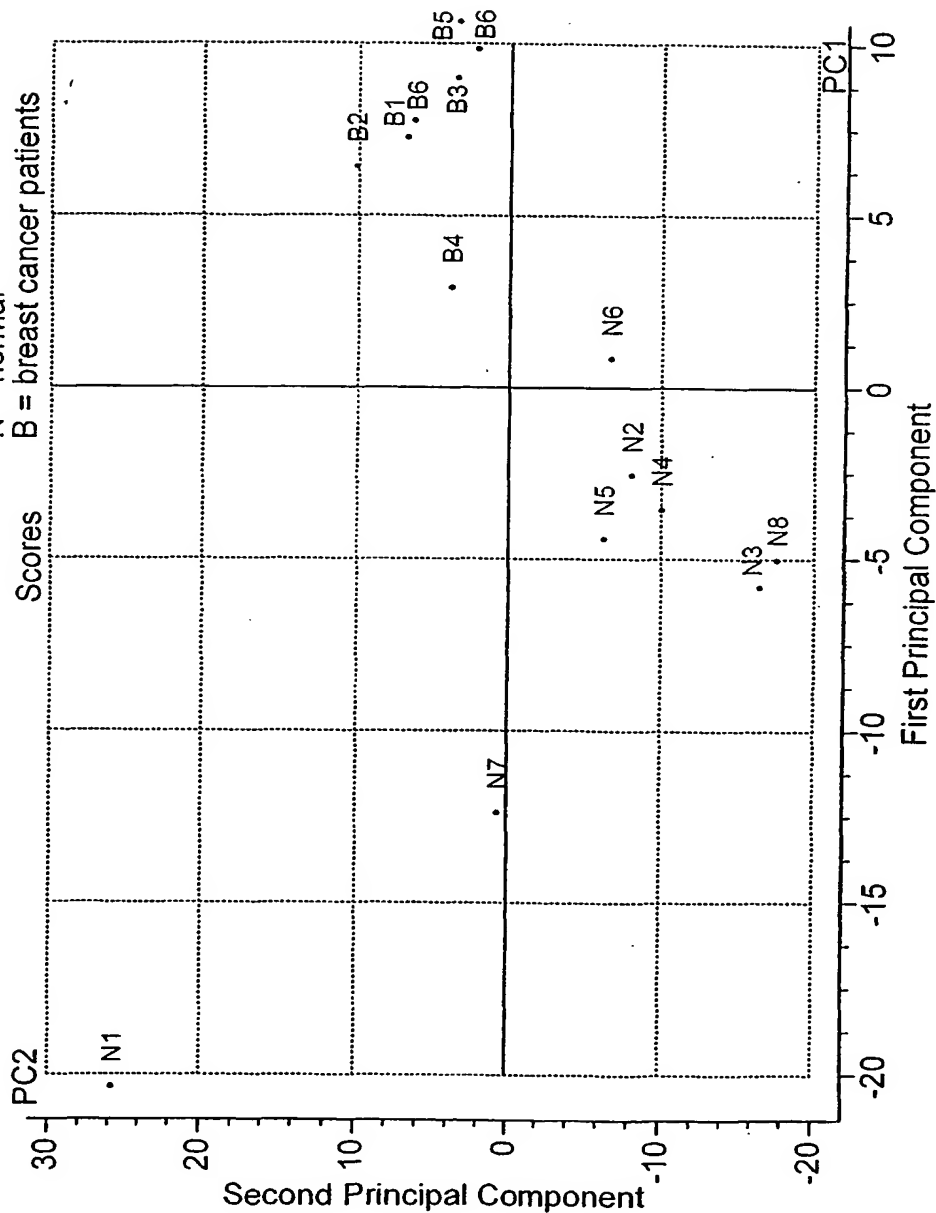PC = Principal Components
N = normal
C = breast cancer patients

Praveen SHARMA et al
PRODUCT AND METHOD
Q-87920

10/535414

WO 2004/046382   PCT/GB2003/005102

4 / 12

FIG. 3

Projection of individuals with and without Alzheimer's disease onto a
classification model generated by PLSR-DA using 182 informative genes.

PC = Principal Components
N = Non –Alzheimer's disease
A = Alzheimer's disease

Praveen SHARMA et al
PRODUCT AND METHOD
Q-87920

10/535414

WO 2004/046382   PCT/GB2003/005102

5 / 12

FIG. 4

Projection of normal (women with suspected mammogram but no breast cancer) and breast cancer samples onto a classification model generated by PLSR-DA using the data of 719 cDNAs
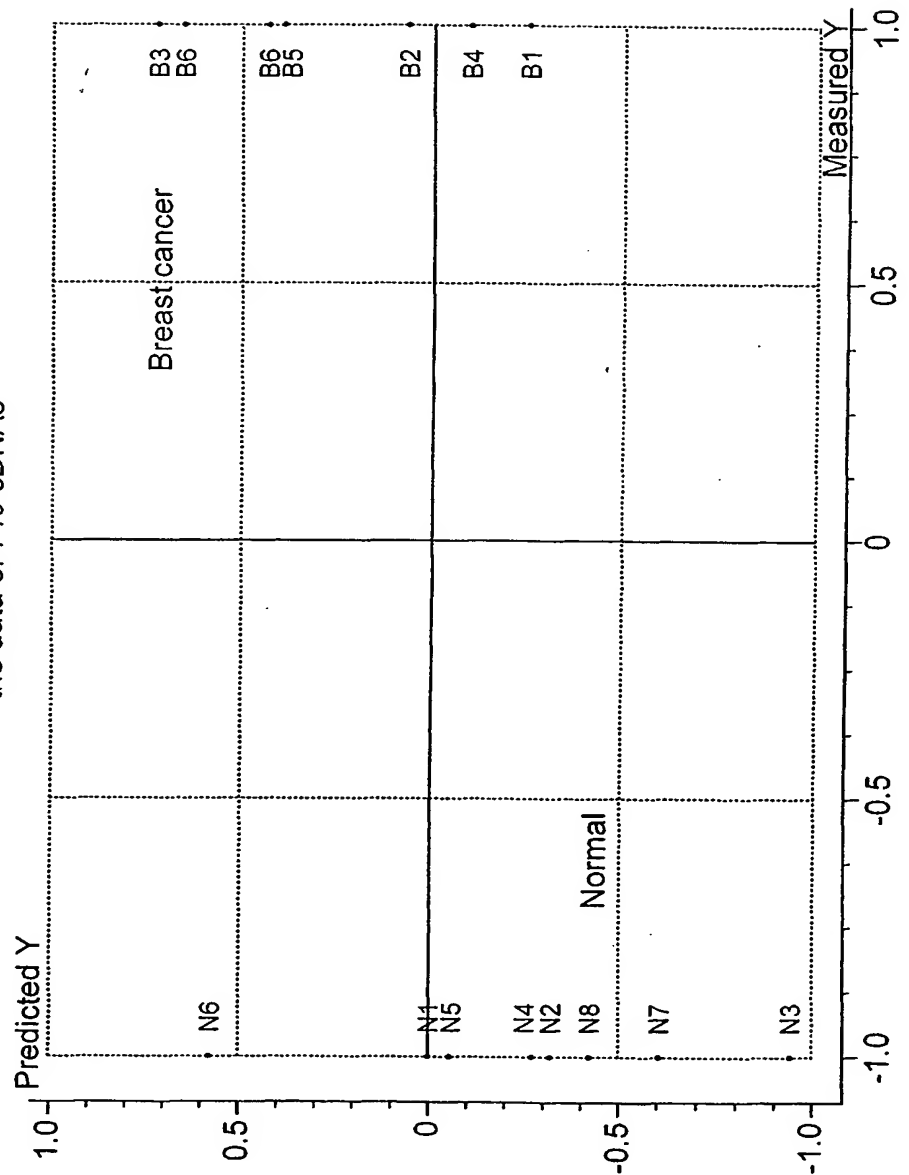
PC = Principal Components
N = normal
B = breast cancer patients

Praveen SHARMA et al
PRODUCT AND METHOD
Q-87920

10/535414

WO 2004/046382

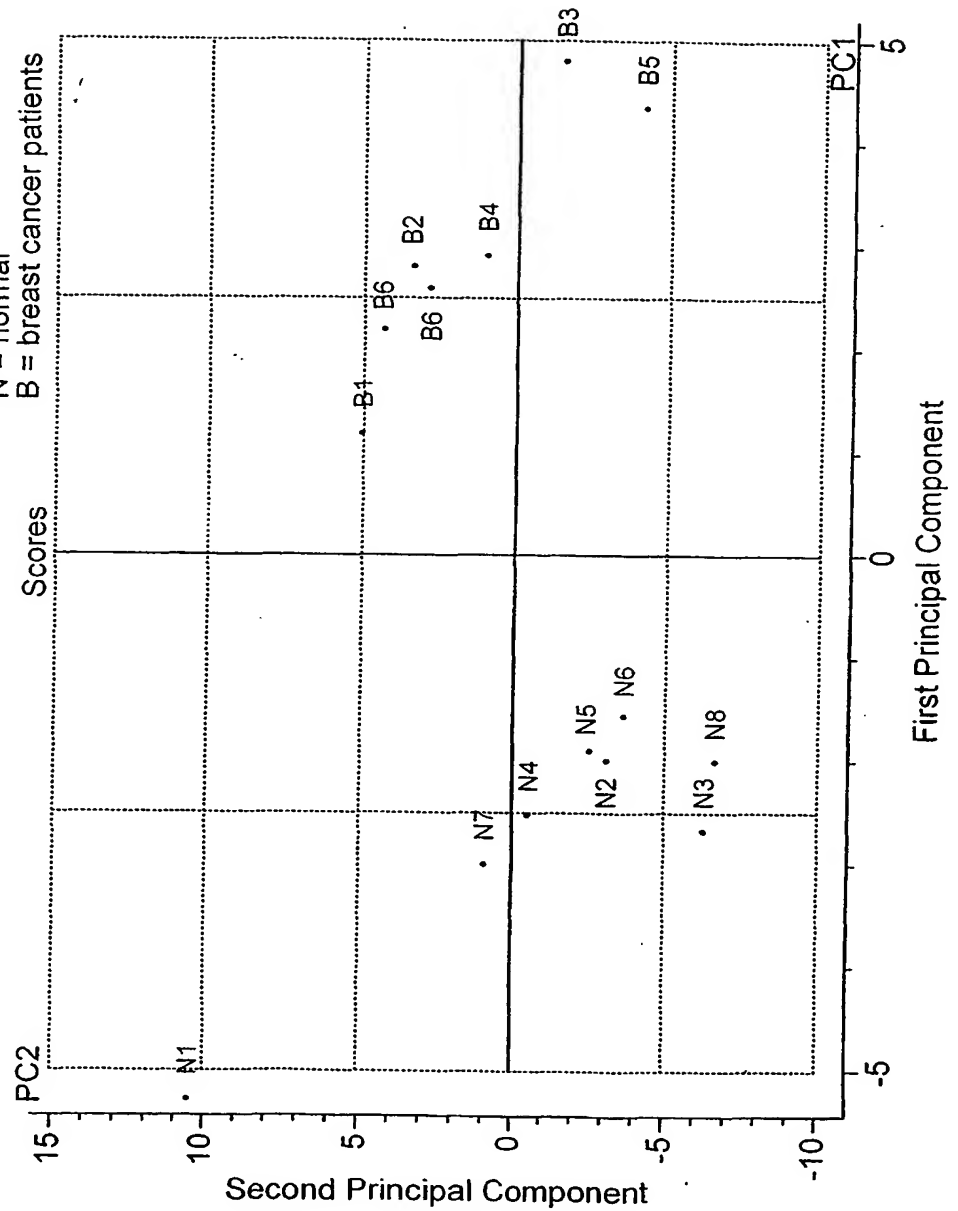PCT/GB2003/005102

6 / 12

FIG. 5

Prediction of normal (women with suspected mammogram but no breast
cancer) and breast cancer samples based on 3 principal components using
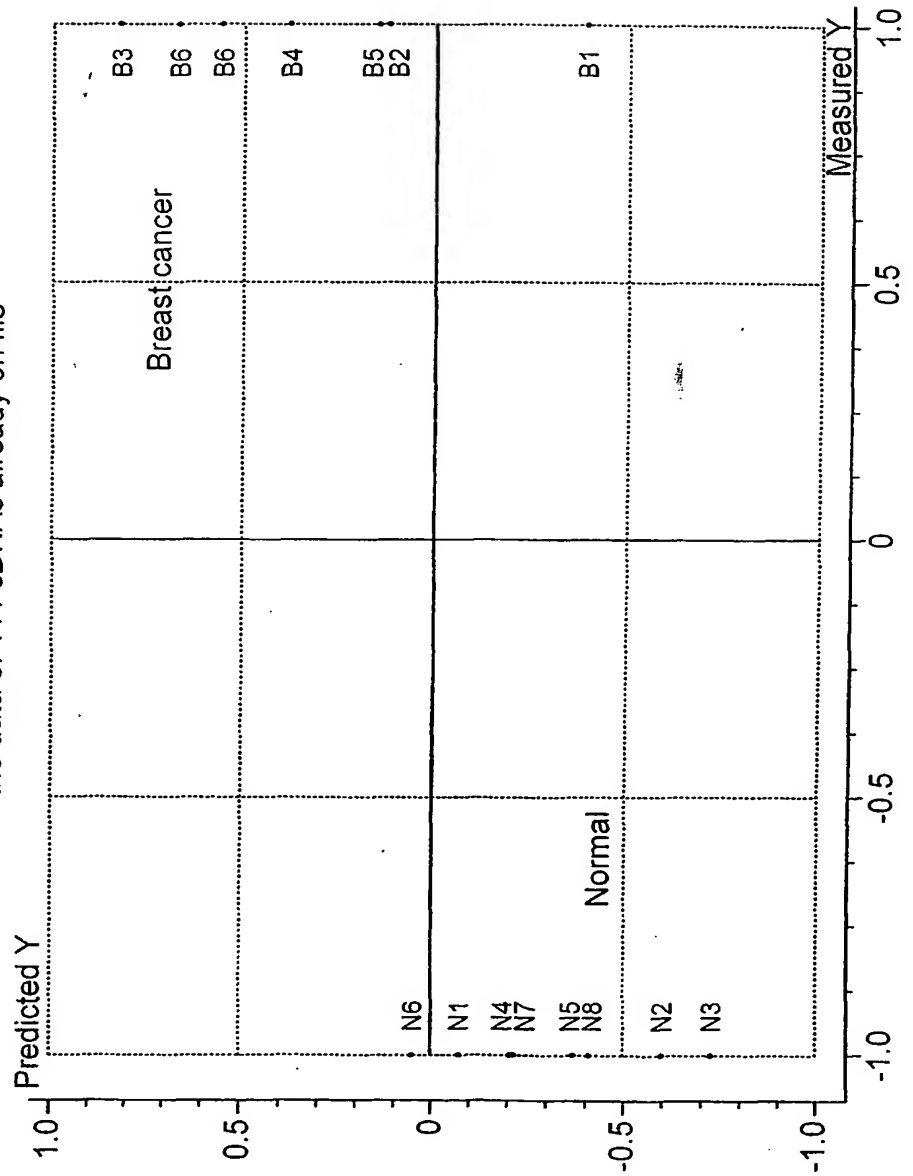the data of 719 cDNAs

7 / 12

FIG. 6

Projection of normal (women with suspected mammogram but no breast
cancer) and breast cancer samples onto a classification model generated by
PLSR-DA using the data of 111 cDNAs already on file

PC = Principal Components
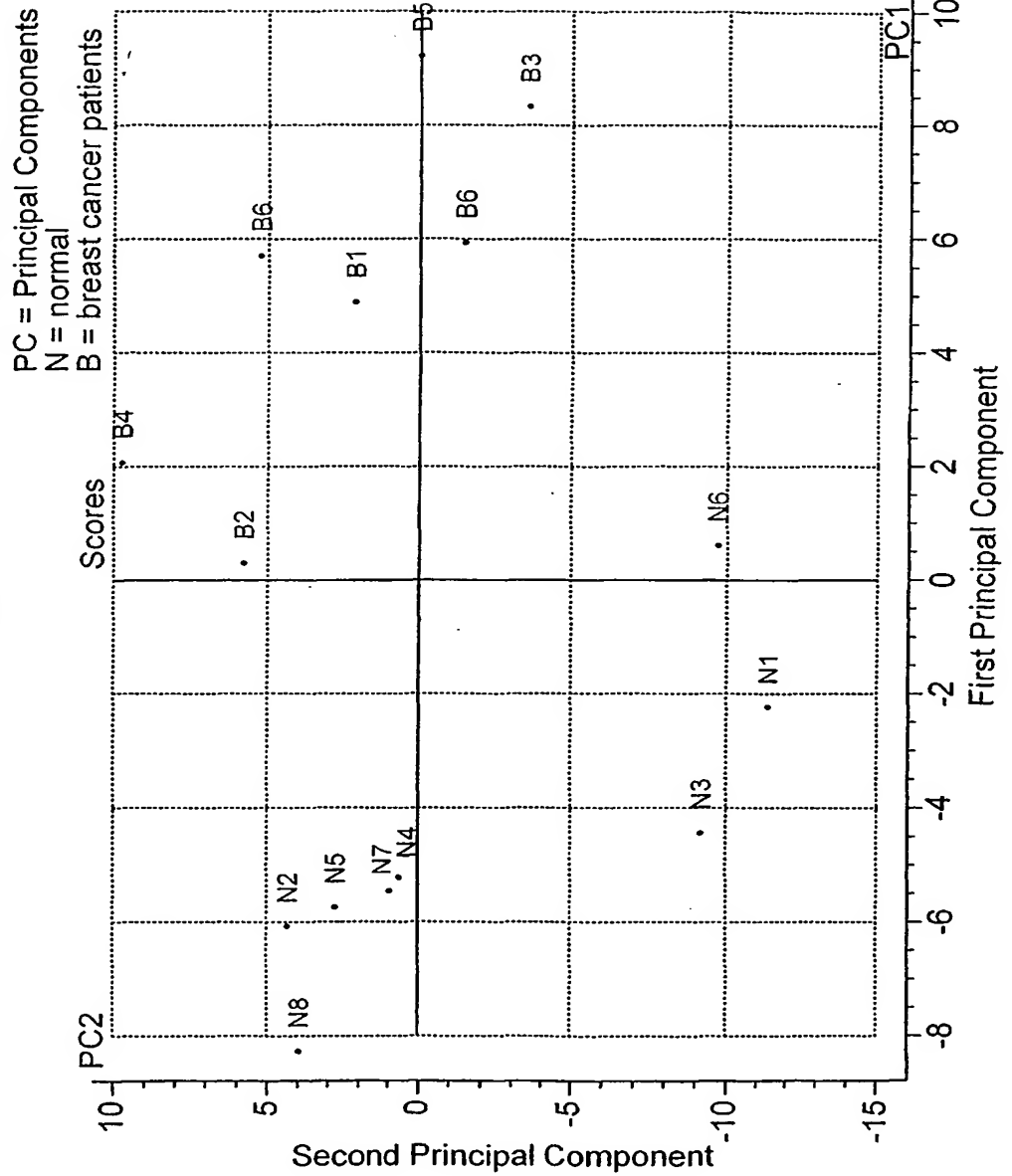N = normal
B = breast cancer patients

Praveen SHARMA et al
PRODUCT AND METHOD
Q-87920

10/535414

WO 2004/046382

PCT/GB2003/005102

8 / 12

FIG. 7

Prediction of normal (women with suspected mammogram but no breast
cancer) and breast cancer samples based on 4 principal components using
the data of 111 cDNAs already on file

10./535414

FIG. 8

Projection of normal (women with suspected mammogram but no breast cancer) and breast cancer samples onto a classification model generated by PLSR-DA using the data of 345 sequenced cDNAs for breast cancer

PC = Principal Components
N = normal
B = breast cancer patients

10/535414

FIG. 9

Prediction of normal (women with suspected mammogram but no breast cancer) and breast cancer samples based on 3 principal components using the data of 345 sequenced cDNAs
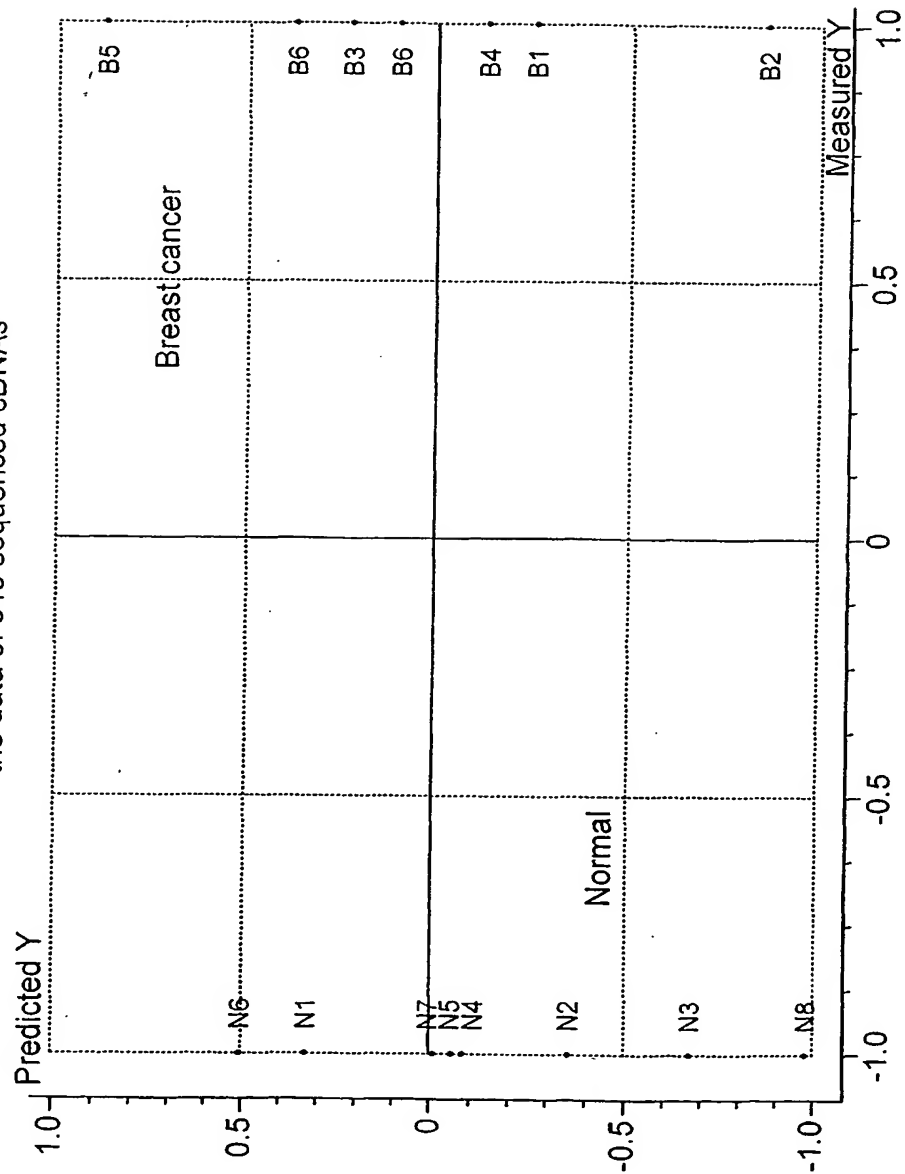
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PRODUCT AND METHOD
Q-87920

10/535414

WO 2004/046382

PCT/GB2003/005102

11 / 12

FIG. 10

Projection of non-alzheimer and alzheimer samples onto a classification
model generated by PLSR-DA using the data of 520 sequenced cDNAs

PC = Principal Components
A = non-alzheimer
AD = alzheimer patients

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PRODUCT AND METHOD
Q-87920

10/535414

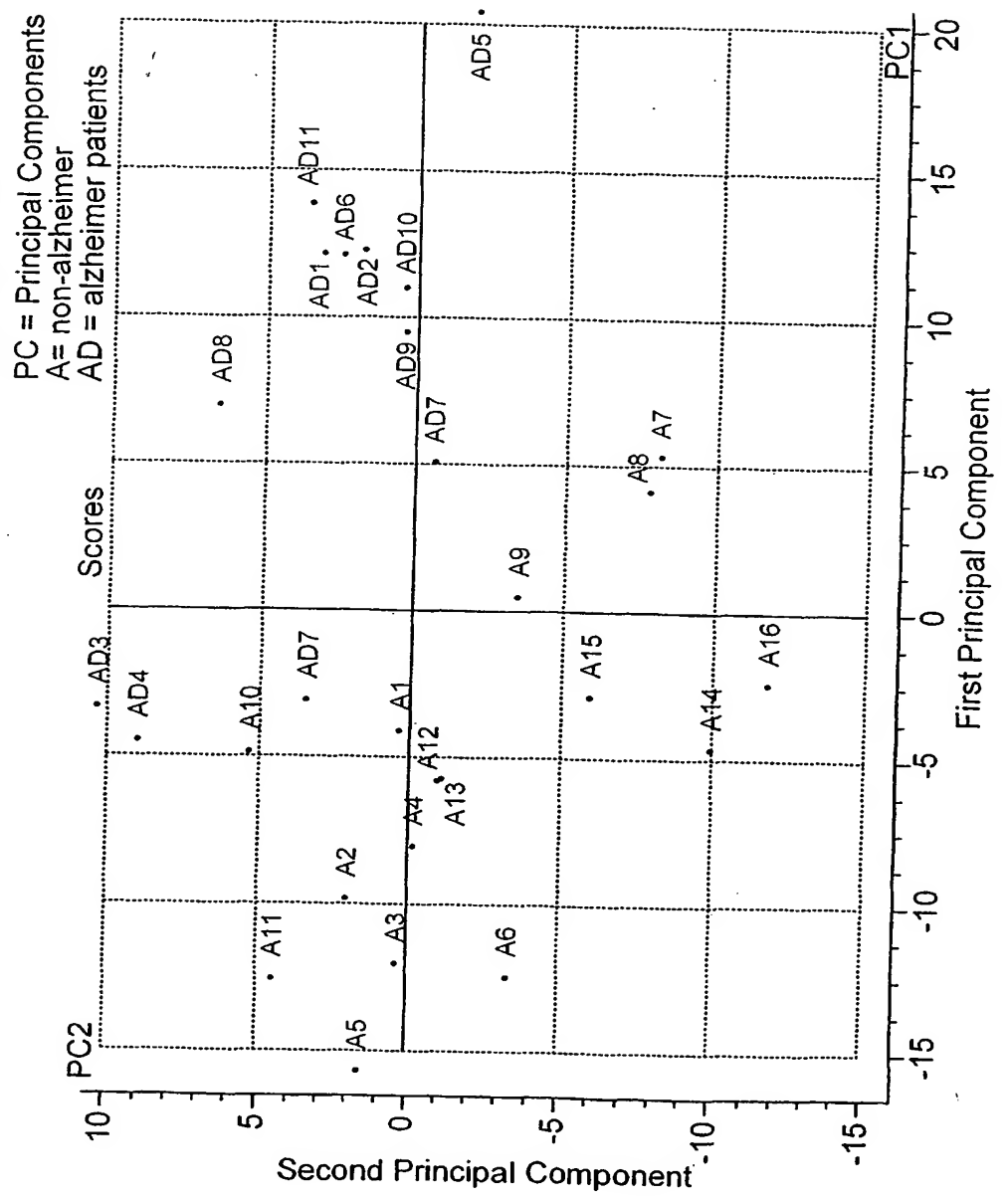WO 2004/046382   PCT/GB2003/005102

12 / 12

FIG. 11

Prediction of non-alzheimer and alzheimer samples based on 4
principal components using the data of sequenced cDNAs